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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:08:53 ; Search time 68.1863 Seconds
(without alignments)
1877.123 Million cell updates/sec

Title: US-09-925-179-8
Perfect score: 2432
Sequence: 1 EVQLVESGGGLVQPGGSLRL.....MHEALHNHYTQKSLSPGK 453

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2432	100.0	453	2 AAR33311	Aar33311 Humanised
2	2432	100.0	453	3 AAY85199	Aay85199 Heavy cha
3	2391	98.3	451	2 AAW95659	Aaw95659 Mus muscu
4	2391	98.3	451	2 AAW95661	Aaw95661 Mus muscu
5	2391	98.3	451	3 AAY85201	Aay85201 Light cha
6	2391	98.3	451	4 AAB47088	Aab47088 Anti-IgE
7	2391	98.3	451	4 AAB76948	Aab76948 Full leng
8	2391	98.3	451	4 AAB76950	Aab76950 Full leng
9	2369	97.4	451	2 AAW95663	Aaw95663 Mus muscu
10	2369	97.4	451	2 AAY50031	Aay50031 Human E27
11	2369	97.4	451	3 AAB07473	Aab07473 Amino aci
12	2369	97.4	451	4 AAB76952	Aab76952 Full leng
13	2369	97.4	451	4 AAB74212	Aab74212 E27 anti-
14	2369	97.4	451	6 ABU62798	Abu62798 E27 anti-
15	2214.5	91.1	452	2 AAY29458	Aay29458 Recombina
16	2214.5	91.1	452	3 AAY77766	Aay77766 Humanised
17	2214.5	91.1	452	3 AAB30322	Aab30322 Humanised
18	2214.5	91.1	452	6 ABU13799	Abu13799 Humanised
19	2214.5	91.1	452	6 ABU59512	Abu59512 Humanised
20	2214.5	91.1	452	7 AAE39094	Aae39094 Protein #
21	2210	90.9	476	5 ABB81110	Abb81110 Anti-VEGF
22	2207.5	90.8	447	6 AAE33522	Aae33522 Human AQC
23	2205.5	90.7	452	2 AAW69316	Aaw69316 Anti-IL-8
24	2204.5	90.6	477	4 AAU14288	Aau14288 Human nov
25	2202.5	90.6	445	6 AAO31101	Aao31101 Human A2-

26	2201.5	90.5	447	6 AAE33523	Aae33523 Human AQC
27	2197.5	90.4	447	6 AAE33524	Aae33524 Human AQC
28	2191	90.1	449	6 ABP58273	Abp58273 Humanised
29	2191	90.1	468	6 ABP58275	Abp58275 Humanised
30	2183.5	89.8	475	2 AAR20057	Aar20057 Heavy cha
31	2182	89.7	449	3 AAY68810	Aay68810 A rat hea
32	2179.5	89.6	449	7 ADB85320	Adb85320 Heavy cha
33	2178	89.6	474	5 AAO14065	Aao14065 Heavy cha
34	2178	89.6	474	6 ABU08017	Abu08017 Human mon
35	2177.5	89.5	444	6 AAE35327	Aae35327 Humanised
36	2177.5	89.5	444	6 AAE34876	Aae34876 BiWA4/8 a
37	2177	89.5	451	4 AAE12715	Aae12715 Human rec
38	2177	89.5	451	6 ABU58807	Abu58807 Mucin 1 (
39	2176.5	89.5	442	6 ABR39465	Abr39465 Humanised
40	2176.5	89.5	442	6 ABU08311	Abu08311 Humanised
41	2176.5	89.5	442	6 ABB80109	Abb80109 Heavy cha
42	2176.5	89.5	461	4 AAU07745	Aau07745 Humanised
43	2176.5	89.5	461	6 ABR39844	Abr39844 Hu266 N56
44	2176.5	89.5	461	6 ABR39847	Abr39847 Hu266 N56
45	2176.5	89.5	461	6 ABR39843	Abr39843 Hu266 N56

ALIGNMENTS

RESULT 1
AAR33311
ID AAR33311 standard; protein; 453 AA.
XX
AC AAR33311;
XX
DT 25-MAR-2003 (revised)
DT 05-JUL-1993 (first entry)
XX
DE Humanised MaE11 Version 1 (intact IgG) heavy chain.
XX
KW Antibody; high affinity; FCEH; low affinity; FCEL; IgE receptor;
KW histamine; mast cell; basophil; Kabat; CDR; murine; MaE11; Fab;
KW humael1v1.
XX
OS Synthetic.
XX
PN WO9304173-A1.
XX
PD 04-MAR-1993.
XX
PF 14-AUG-1992; 92WO-US006860.
XX
PR 14-AUG-1991; 91US-00744768.
PR 07-MAY-1992; 92US-00879495.
XX
PA (GETH) GENENTECH INC.
XX
PI Jardieu PM, Presta LG;
XX
DR WPI; 1993-094004/11.
XX
PT Polypeptide(s) binding to specific Fc epsilon receptors - act as IgE
PT antagonists; useful for treating and preventing IgE-mediated disorders
PT e.g. allergies.
XX
PS Example 4; Fig 3; 113pp; English.
XX
CC Residues were selected from MaE11 and inserted or substituted into a
CC human Fab antibody background (Vh region Kabat subgroup III and VI region
CC kappa subgroup I). A first version, humael1v1 or version 1 is given
CC below. The affinity of version 1 was assayed and found to be ca. 100
CC times lower than that of the donor antibody MaE11. Therefore, further
CC modifications in the sequence of version 1 were made. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 453 AA;

Query Match 100.0%; Score 2432; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 6.6e-142;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVDSGGGLVQPGGSLRLSCAIVSGYSITSGYWNWIRQAPGKLEWVASITYDGSNTY 60
|||
Db 1 EVQLVDSGGGLVQPGGSLRLSCAIVSGYSITSGYWNWIRQAPGKLEWVASITYDGSNTY 60
|||

Qy 61 ADSVKGRTISRDDSKNTFYLMNSLRADTAIVYICARGSHYFGHWHFAVWGQGLTVTS 120
|||
Db 61 ADSVKGRTISRDDSKNTFYLMNSLRADTAIVYICARGSHYFGHWHFAVWGQGLTVTS 120
|||

Qy 121 SASTKGKPSVFPLAPSSKTSISGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
|||
Db 121 SASTKGKPSVFPLAPSSKTSISGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
|||

Qy 181 QSSGLYSLSVVTVPSSSLGTQYICNVNHNKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 240
|||
Db 181 QSSGLYSLSVVTVPSSSLGTQYICNVNHNKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 240
|||

Qy 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
|||
Db 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
|||

Qy 301 QYNSTYRVVSVLTVHLQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
|||
Db 301 QYNSTYRVVSVLTVHLQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
|||

Qy 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDK 420
|||
Db 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDK 420
|||

Qy 421 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453
|||
Db 421 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453
|||

RESULT 2
AAW85199
ID AAW85199 standard; protein; 453 AA.
XX
AC AAW85199;
XX
DT 29-JUN-2000 (first entry)
XX
DE Heavy chain amino acid sequence of the humanised MaE11 antibody.
XX
KW Immunoglobulin E; IgE; anti-human IgE; bispecific antibody; FCEL; FCEH;
KW low affinity binding receptor; high affinity binding receptor; allergy;
KW diagnosis; treatment; histamine release; heavy chain; prevent; chimeric.
XX
OS Mus sp.
OS Homo sapiens.
XX
PN US6037453-A.
XX
PD 14-MAR-2000.
XX
PF 06-JUN-1995; 95US-00466151.
XX
PR 14-AUG-1992; 92WO-US006860.
PR 26-JAN-1994; 94US-00185899.
PR 15-MAR-1995; 95US-00405617.
XX
PA (GETH) GENENTECH INC.
XX
PI Presta LG, Jardieu PM;
XX
XX WPI; 2000-269913/23.
DR
XX New bispecific antibodies, useful for treating immunoglobulin E-mediated
PT disease, binds to IgE, but only when on the low affinity receptor, and to
PT an antigen other than IgE.

XX
PS
XX Claim 14; Fig 3; 48pp; English.
CC This sequence represents the heavy chain amino acid sequence of a
CC humanised mouse anti-human immunoglobulin E (IgE) antibody. The invention
CC relates to a bispecific antibody that binds specifically to IgE when IgE
CC is bound to its low affinity receptor (FCEL), but does not bind to IgE,
CC when IgE is bound to its high affinity receptor (FCEH). The bispecific
CC antibody comprises an IgE-binding arm with human framework residues of a
CC recipient human antibody and donor murine CDR (complementarity
CC determining region) residues, but with at least one human CDR residue
CC replacing the analogous murine residue. The antibody also comprises an Fv
CC that is specific for a predetermined antigen other than IgE. The
CC antibodies work by displacing bound IgE from its receptor, or via
CC competitive inhibition of its binding. The bispecific antibodies are used
CC for diagnosis, treatment and prevention of allergy and other IgE-mediated
CC diseases, also, when immobilised, for the isolation of FCEL from cells
CC (for research or therapy). The bispecific antibodies of the invention do
CC not cause granulation or release of histamine from mast cells
XX
SQ Sequence 453 AA;
Query Match 100.0%; Score 2432; DB 3; Length 453;
Best Local Similarity 100.0%; Pred. No. 6.6e-142;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYWNWIRQAPGKLEWVASITYDGSNTY 60
|||
Db 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYWNWIRQAPGKLEWVASITYDGSNTY 60
|||

Qy 61 ADSVKGRTISRDDSKNTFYLMNSLRADTAIVYICARGSHYFGHWHFAVWGQGLTVTS 120
|||
Db 61 ADSVKGRTISRDDSKNTFYLMNSLRADTAIVYICARGSHYFGHWHFAVWGQGLTVTS 120
|||

Qy 121 SASTKGKPSVFPLAPSSKTSISGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
|||
Db 121 SASTKGKPSVFPLAPSSKTSISGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
|||

Qy 181 QSSGLYSLSVVTVPSSSLGTQYICNVNHNKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 240
|||
Db 181 QSSGLYSLSVVTVPSSSLGTQYICNVNHNKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 240
|||

Qy 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
|||
Db 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
|||

Qy 301 QYNSTYRVVSVLTVHLQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
|||
Db 301 QYNSTYRVVSVLTVHLQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
|||

Qy 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDK 420
|||
Db 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDK 420
|||

Qy 421 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453
|||
Db 421 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453
|||

RESULT 3
AAW95659
ID AAW95659 standard; protein; 451 AA.
XX
AC AAW95659;
XX
DT 08-JUN-1999 (first entry)
XX
DE Mus musculus anti-IgE e25 full length variable heavy chain.
XX
KW Heavy chain; IgE; antibody; anti-IgE; reduction; prevention; histamine;
KW production; hypersensitivity; allergen; anaphylaxis; atopic allergy;
KW asthma; allergic rhinitis; conjunctivitis; hay fever; eczema;
KW anaphylactic shock; urticaria.

XX OS Mus musculus.
XX PN WO9901556-A2.
XX PD 14-JAN-1999.
XX PF 30-JUN-1998; 98WO-US013410.
XX PR 02-JUL-1997; 97US-00887352.
XX PA (GETH) GENENTECH INC.
XX PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX DR WPI; 1999-106057/09.
XX PT Improving affinity of polypeptides, particularly anti-IgE antibodies - by
PT identifying aspartyl residues which undergo isomerisation and
PT substituting alternative residues and screening for affinity against the
PT target.
XX PS Disclosure; Page 92-94; 129pp; English.
XX CC The sequence is that of thefull length heavy chain of e25. It was used as
CC part of a method to improve the affinity of anti-IgE antibodies such as
CC e26 and e27. The e26 and e27 antibodies can be used for reducing or
CC preventing IGE mediated production of histamine in a mammal. They can be
CC used for treating a disorder mediated by IGE such as hypersensitivity,
CC atopic allergy, asthma, allergic rhinitis, conjunctivitis, hay fever,
CC eczema, anaphylactic shock and urticaria. The antibodies can also be used
CC for affinity purification, detection and diagnosis
XX SQ Sequence 451 AA;
Query Match 98.3%; Score 2391; DB 2; Length 451;
Best Local Similarity 98.9%; Pred. No. 2.2e-139;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
QY 1 EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSWNWIRQAPGKLEWVASITYDGS TNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSWNWIRQAPGKLEWVASITYDGS TNY 60
QY 61 ADSVKGRFTISRDDSKNTFY LQMNSLRAEDTAVYYCARGSHYFGHWHPAVWGQTLVTVS 120
Db 61 NPSVKGRITISRDDSKNTFY LQMNSLRAEDTAVYYCARGSHYFGHWHPAVWGQTLVTVS 120
QY 121 SASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSSVTVTPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238
QY 241 LGGPSVFLFPPKPKD TLMISRTPETCVTVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLFPPKPKD TLMISRTPETCVTVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY 301 QYNSTYRVVSVLT V LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db 299 QYNSTYRVVSVLT V LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQQGNVFSCSVNHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQQGNVFSCSVNHEALHNHYTQKSLSLSPGK 451

AAW95661
ID AAW95661 standard; protein; 451 AA.
XX AC AAW95661;
XX DT 08-JUN-1999 (first entry)
XX DE Mus musculus anti-IgE e26 full length heavy chain.
XX KW Heavy chain; IgE; antibody; anti-IgE; reduction; prevention; histamine;
KW production; hypersensitivity; allergen; anaphylaxis; atopic allergy;
KW asthma; allergic rhinitis; conjunctivitis; hay fever; eczema;
KW anaphylactic shock; urticaria.
XX OS Mus musculus.
XX PN WO9901556-A2.
XX PD 14-JAN-1999.
XX PF 30-JUN-1998; 98WO-US013410.
XX PR 02-JUL-1997; 97US-00887352.
XX PA (GETH) GENENTECH INC.
XX PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX DR WPI; 1999-106057/09.
XX PT Improving affinity of polypeptides, particularly anti-IgE antibodies - by
PT identifying aspartyl residues which undergo isomerisation and
PT substituting alternative residues and screening for affinity against the
PT target.
XX PS Disclosure; Page 95-96; 129pp; English.
XX CC The sequence is that of the full length heavy chain of e26. It was used
CC as part of a method to improve the affinity of anti-IgE antibodies such
CC as e26 and e27. The e26 and e27 antibodies can be used for reducing or
CC preventing IGE mediated production of histamine in a mammal. They can be
CC used for treating a disorder mediated by IGE such as hypersensitivity,
CC atopic allergy, asthma, allergic rhinitis, conjunctivitis, hay fever,
CC eczema, anaphylactic shock and urticaria. The antibodies can also be used
CC for affinity purification, detection and diagnosis
XX SQ Sequence 451 AA;
Query Match 98.3%; Score 2391; DB 2; Length 451;
Best Local Similarity 98.9%; Pred. No. 2.2e-139;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
QY 1 EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSWNWIRQAPGKLEWVASITYDGS TNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSWNWIRQAPGKLEWVASITYDGS TNY 60
QY 61 ADSVKGRFTISRDDSKNTFY LQMNSLRAEDTAVYYCARGSHYFGHWHPAVWGQTLVTVS 120
Db 61 NPSVKGRITISRDDSKNTFY LQMNSLRAEDTAVYYCARGSHYFGHWHPAVWGQTLVTVS 120
QY 121 SASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSSVTVTPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238
QY 241 LGGPSVFLFPPKPKD TLMISRTPETCVTVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLFPPKPKD TLMISRTPETCVTVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY 301 QYNSTYRVVSVLT V LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360

Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 5
AAY85201
ID AAY85201 standard; protein; 451 AA.
XX
AC AAY85201;
XX
DT 29-JUN-2000 (first entry)
XX

DE Light chain amino acid sequence of anti-human IgE antibody.
XX
KW Immunoglobulin E; IgE; anti-human IgE; bispecific antibody; FCEL; FCEH;
KW low affinity binding receptor; high affinity binding receptor; allergy;
KW diagnosis; treatment; histamine release; heavy chain; prevent.
XX
OS Mus sp.

XX
PN US6037453-A.
XX
PD 14-MAR-2000.
XX
PF 06-JUN-1995; 95US-00466151.
XX
PR 14-AUG-1992; 92WO-US006860.
PR 26-JAN-1994; 94US-00185899.
PR 15-MAR-1995; 95US-00405617.

XX (GETH) GENENTECH INC.
XX
PI Presta LG, Jardieu PM;
XX
DR WPI; 2000-269913/23.
XX

PT New bispecific antibodies, useful for treating immunoglobulin E-mediated
PT disease, binds to IgE, but only when on the low affinity receptor, and to
PT an antigen other than IgE.

XX
PS Claim 15; Col 73-76; 48pp; English.
XX

CC This sequence represents the light chain amino acid sequence of a mouse
CC anti-human immunoglobulin E (IgE) antibody. The invention relates to a
CC bispecific antibody that binds specifically to IgE when IgE is bound to
CC its low affinity receptor (FCEL), but does not bind to IgE, when IgE is
CC bound to its high affinity receptor (FCEH). The bispecific antibody
CC comprises an IgE-binding arm with human framework residues of a recipient
CC human antibody and donor murine CDR (complementarity determining region)
CC residues, but with at least one human CDR residue replacing the analogous
CC murine residue. The antibody also comprises an Fv that is specific for a
CC predetermined antigen other than IgE. The antibodies work by displacing
CC bound IgE from its receptor, or via competitive inhibition of its
CC binding. The bispecific antibodies are used for diagnosis, treatment and
CC prevention of allergy and other IgE-mediated diseases, also, when
CC immobilised, for the isolation of FCEL from cells (for research or
CC therapy). The bispecific antibodies of the invention do not cause
CC granulation or release of histamine from mast cells
XX

SQ Sequence 451 AA;

Query Match 98.3%; Score 2391; DB 3; Length 451;
Best Local Similarity 98.9%; Pred. No. 2.2e-139;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASITYDGSTNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASITYDGSTNY 60
QY 61 ADSVKGRFTISRDDSKNTFYIQMNSLRAEDTAVYICARGSHYFGHHFAVWGQGLVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYIQMNSLRAEDTAVYICARGSHYFGHHFAVWGQGLVTVS 120
QY 121 SASTKGKPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSVVTVPSSSLGFTQYICNVNHPKPSNTKYDKKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSVVTVPSSSLGFTQYICNVNHPKPSNTKYDKKVEPKSCDKTHTCPPCPAPEL 238
QY 241 LGGPSVFLFPPPKPDKTLISRTPPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREE 300
Db 239 LGGPSVFLFPPPKPDKTLISRTPPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREE 298
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 6

AAB47088

ID AAB47088 standard; protein; 451 AA.

XX

AC AAB47088;

XX

DT 11-SEP-2003 (revised)

DT 08-MAY-2001 (first entry)

XX

DE Anti-IgE antibody, E26, heavy chain.

XX

KW Light chain; heavy chain; anti-IgE antibody; E26; transfection;
KW green fluorescent protein; GFP; promoter; expression.

XX

OS Homo sapiens.

OS Mus musculus.

OS Chimeric.

XX WO200104306-A1.
XX

PD 18-JAN-2001.
XX

PF 11-JUL-2000; 2000WO-US018841.
XX

PR 12-JUL-1999; 99US-0143360P.
XX

PA (GETH) GENENTECH INC.
XX

PI Chisholm V, Crowley CW, Krummen LA, Meng YG;
XX

DR WPI; 2001-138352/14.
XX

PT Novel polynucleotide construct for screening and obtaining cells
PT expressing high levels of desired protein, comprises amplifiable
PT selectable gene, fluorescent protein gene and sequence encoding desired
PT product.

XX Disclosure; Fig 13B; 75pp; English.

XX The sequences given in AAB47087-88 represent the light and heavy chains
CC

CC of the anti-IgE antibody, E26. These sequences were expressed by the
CC construct of the invention, which comprises an amplifiable selectable
CC gene, a green fluorescent protein gene (GFP), and a selected sequence
CC encoding a desired product, which is operably linked to either the
CC amplifiable selectable gene or to the GFP gene, and to a promoter.
CC Constructs such as this, are useful for producing a desired product by
CC introduction into a suitable eukaryotic cell, culturing the resultant
CC eukaryotic cell under conditions so as to express the desired product,
CC and recovering the desired product from the culture medium. The
CC constructs are efficient for identifying and selecting for stable
CC eukaryotic cells expressing high levels of a desired product. They are
CC suitable for earlier and faster screening of transfected cells. (Updated
CC on 11-SEP-2003 to standardise OS field)

XX Sequence 451 AA;

Query Match 98.3%; Score 2391; DB 4; Length 451;
Best Local Similarity 98.9%; Pred. No. 2.2e-139;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKLEWVASITYDGSNTY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKLEWVASITYDGSNTY 60
QY 61 ADSVKGRFTISRDDSKNTFYQLQMSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYQLQMSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120
QY 121 SASTKGKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSSVTVPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSSVTVPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238
QY 241 LGGPSVFLFPPKPKDITLMISRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLFPPKPKDITLMISRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQQGNVFSCSVNHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQQGNVFSCSVNHEALHNHYTQKSLSLSPGK 451

RESULT 7

AAB76948

ID AAB76948 standard; protein; 451 AA.

XX AAB76948;

AC AAB76948;

XX 17-APR-2001 (first entry)

DT 17-APR-2001 (first entry)

XX Full length heavy chain sequence of e25 SEQ ID 14.

DE Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;

XX Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;

KW antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;

KW conjunctivitis; eczema; urticaria; food allergy.

XX Synthetic.

OS Synthetic.

XX US6172213-B1.

PN US6172213-B1.

XX 09-JAN-2001.

PD 09-JAN-2001.

XX

PF 30-JUN-1998; 98US-00109207.

XX 02-JUL-1997; 97US-0051554P.

PR (GETH) GENENTECH INC.

XX Lowman HB, Presta LG, Jardieu PM, Lowe J;

XX WPI; 2001-122353/13.

XX New nucleic acid encoding anti-immunoglobulin E antibody with improved

PT properties, produced by substituting aspartyl residues in unimproved

PT immunoglobulin E prone to isomerization by other residues by affinity

PT maturation with phage display.

XX Disclosure; Fig 12; 87pp; English.

XX This invention relates to a nucleotide sequence encoding an antibody with

CC improved anti-IgE antibody activity. The antibody has improved action due

CC to a process comprising, a) identifying aspartyl residues prone to

CC isomerisation in unimproved anti-IgE (immunoglobulin E) antibody; b)

CC substituting alternative residues to create candidate molecules, and c)

CC selecting those candidate molecules which display affinity against the

CC target molecule. Use of the antibody results in antiasthmatic;

CC antiallergic; ophthalmological; dermatological and antiinflammatory

CC activity. The antibodies are useful for treating IgE-mediated disorders

CC such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and

CC food allergies. The mutant antibodies produced by the above mentioned

CC nucleic acids may also be used as affinity purification agents and in

CC diagnostic assays for detecting the expression of an antigen of interest

CC in specific cell, tissues or serum. Amino acid sequences AAB76936-

CC AAB76960 represent fragments of anti-IgE antibodies of the invention.

CC Polynucleotide sequence AAF69253 represents an expression plasmid used in

CC the course of the invention, and oligonucleotides AAF69254 - AAF69271 are

CC used in the generation of affinity improved anti-IgE antibodies

XX Sequence 451 AA;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKLEWVASITYDGSNTY 60

Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKLEWVASITYDGSNTY 60

QY 61 ADSVKGRFTISRDDSKNTFYQLQMSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120

Db 61 NPSVKGRITISRDDSKNTFYQLQMSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120

QY 121 SASTKGKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180

Db 121 SAST--KGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178

QY 181 QSSGLYSLSSVTVPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240

Db 179 QSSGLYSLSSVTVPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238

QY 241 LGGPSVFLFPPKPKDITLMISRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300

Db 239 LGGPSVFLFPPKPKDITLMISRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360

Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358

QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420

Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418

QY 421 SRWQQGNVFSCSVNHEALHNHYTQKSLSLSPGK 453

Db 419 SRWQQGNVFSCSVNHEALHNHYTQKSLSLSPGK 451

Query Match 98.3%; Score 2391; DB 4; Length 451;

Best Local Similarity 98.9%; Pred. No. 2.2e-139;

Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

RESULT 8
AAB76950
ID AAB76950 standard; protein; 451 AA.
XX
AC AAB76950;
XX
DT 17-APR-2001 (first entry)
XX
DE Full length heavy chain sequence of e26 SEQ ID 16.
XX
KW Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
KW antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
KW conjunctivitis; eczema; urticaria; food allergy.
XX
OS Synthetic.
XX
FN US6172213-B1.
XX
PD 09-JAN-2001.
XX
PF 30-JUN-1998; 98US-00109207.
XX
PR 02-JUL-1997; 97US-0051554P.
XX
PA (GETH) GENENTECH INC.
XX
PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX
DR WPI; 2001-122353/13.
XX
PT New nucleic acid encoding anti-immunoglobulin E antibody with improved
PT properties, produced by substituting aspartyl residues in unimproved
PT immunoglobulin E prone to isomerization by other residues by affinity
PT maturation with phage display.
XX
PS Claim 2; Fig 12; 87pp; English.
XX
CC This invention relates to a nucleotide sequence encoding an antibody with
CC improved anti-IgE antibody activity. The antibody has improved action due
CC to a process comprising, a) identifying aspartyl residues prone to
CC isomerisation in unimproved anti-IgE (immunoglobulin E) antibody; b)
CC substituting alternative residues to create candidate molecules, and c)
CC selecting those candidate molecules which display affinity against the
CC target molecule. Use of the antibody results in antiasthmatic;
CC antiallergic; ophthalmological; dermatological and antiinflammatory
CC activity. The antibodies are useful for treating IgE-mediated disorders
CC such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and
CC food allergies. The mutant antibodies produced by the above mentioned
CC nucleic acids may also be used as affinity purification agents and in
CC diagnostic assays for detecting the expression of an antigen of interest
CC in specific cell, tissues or serum. Amino acid sequences AAB76936-
CC AAB76960 represent fragments of anti-IgE antibodies of the invention.
CC Polynucleotide sequence AAF69253 represents an expression plasmid used in
CC the course of the invention, and oligonucleotides AAF69254 - AAF69271 are
CC used in the generation of affinity improved anti-IgE antibodies
XX
SQ Sequence 451 AA;

Query Match 98.3%; Score 2391; DB 4; Length 451;
Best Local Similarity 98.9%; Pred. No. 2.2e-139;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
QY 61 ADSVKGRFTISRDDSKNTFY LQMSNLSRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFY LQMSNLSRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTVS 120
QY 121 SASTKGKGPSVFPFLAPSSKSTGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVL 180

Db 121 SAST--KGPSVFPFLAPSSKSTGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSSVWTVVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSSVWTVVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238
QY 241 LGGPSVELFPPKPKD TLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVELFPPKPKD TLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY 301 QYNSTYRVVSVLT VLVHQQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db 299 QYNSTYRVVSVLT VLVHQQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 453
Db 419 SRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 451

RESULT 9
AAW95663
ID AAW95663 standard; protein; 451 AA.
XX
AC AAW95663;
XX
DT 08-JUN-1999 (first entry)
XX
DE Mus musculus anti-IgE e27 full length heavy chain.
XX
KW Heavy chain; IgE; antibody; anti-IgE; reduction; prevention; histamine;
KW production; hypersensitivity; allergen; anaphylaxis; atopic allergy;
KW asthma; allergic rhinitis; conjunctivitis; hay fever; eczema;
KW anaphylactic shock; urticaria.
XX
OS Mus musculus.
XX
PN WO9901556-A2.
XX
PD 14-JAN-1999.
XX
PF 30-JUN-1998; 98WO-US013410.
XX
PR 02-JUL-1997; 97US-00887352.
XX
PA (GETH) GENENTECH INC.
XX
PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX
DR WPI; 1999-106057/09.
XX
PT Improving affinity of polypeptides, particularly anti-IgE antibodies - by
PT identifying aspartyl residues which undergo isomerisation and
PT substituting alternative residues and screening for affinity against the
PT target.
XX
PS Disclosure; Page 97-99; 129pp; English.
XX
CC The sequence is that of the full length heavy chain of e27. It was used
CC as part of a method to improve the affinity of anti-IgE antibodies such
CC as e26 and e27. The e26 and e27 antibodies can be used for reducing or
CC preventing IgE mediated production of histamine in a mammal. They can be
CC used for treating a disorder mediated by IgE such as hypersensitivity,
CC atopic allergy, asthma, allergic rhinitis, conjunctivitis, hay fever,
CC eczema, anaphylactic shock and urticaria. The antibodies can also be used
XX for affinity purification, detection and diagnosis
SQ Sequence 451 AA;

OS Synthetic.
XX WO200042072-A2.
PN 20-JUL-2000.
XX 14-JAN-2000; 2000WO-US0000973.
PD 15-JAN-1999; 99US-0116023P.
XX (GETH) GENENTECH INC.
XX Presta LG;
PI WPI; 2000-476035/41.
XX New Fc region-containing polypeptides that have altered effector function
PT due to one or more amino acid modifications in the Fc region, useful in
PT the treatment of cancer and allergic conditions such as asthma.
XX Disclosure; Fig 4B; 132pp; English.
XX The present sequence represents the E27 and anti-IgE antibody heavy
CC chain. The protein is used to produce Fc region-containing polypeptides
CC that have altered effector function as a consequence of one or more amino
CC acid modifications in the Fc region. The variant polypeptides are useful
CC for treating cancer, allergic conditions such as asthma (with an anti-IgE
CC antibody), and LFA-1-mediated disorders. Where the polypeptide binds the
CC HER2 receptor, the disorder preferably is HER2-expressing cancer, e.g. a
CC benign or malignant tumour characterized by overexpression of the HER2
CC receptor. Such cancers include breast cancer, squamous cell cancer, small
CC -cell lung cancer, non-small cell lung cancer, gastrointestinal cancer,
CC pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, bladder
CC cancer, hepatoma, colon cancer, colorectal cancer, endometrial carcinoma,
CC salivary gland carcinoma, kidney cancer, liver cancer, prostate cancer,
CC vulval cancer, thyroid cancer, hepatic carcinoma and various types of
CC head and neck cancer
XX
SQ Sequence 451 AA;

Query Match 97.4%; Score 2369; DB 3; Length 451;
Best Local Similarity 98.0%; Pred. No. 5e-138;
Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

QY 1 EVQLVSGGGLVQPGGSLRLSCAVSGYSITSGYSWNIQAPGKGLEWVASITYDGSTNY 60
Db 1 EVQLVSGGGLVQPGGSLRLSCAVSGYSITSGYSWNIQAPGKGLEWVASIKYGETKY 60
QY 61 ADSVKGRFTISRDDSKNTFYLQWNSLRAEDTAVYYCARGSHYFGHHFAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLQWNSLRAEDTAVYYCARGSHYFGHHFAVWGQGLTVTVS 120
QY 121 SASTKGKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSVWTVPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSVWTVPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238
QY 241 LGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREE 300
Db 239 LGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREE 298
QY 301 QYNSTYRVVSVLTVHLQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db 299 QYNSTYRVVSVLTVHLQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453

Db 419 SRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
RESULT 12
AAB76952
ID AAB76952 standard; protein; 451 AA.
XX AC AAB76952;
XX 17-APR-2001 (first entry)
DT Full length heavy chain sequence of e27 SEQ ID 18.
DE
XX Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
KW antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
KW conjunctivitis; eczema; urticaria; food allergy.
XX Synthetic.
OS
XX US6172213-B1.
PN 09-JAN-2001.
XX 30-JUN-1998; 98US-00109207.
PF 02-JUL-1997; 97US-0051554P.
XX (GETH) GENENTECH INC.
PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX WPI; 2001-122353/13.
DR New nucleic acid encoding anti-immunoglobulin E antibody with improved
XX properties, produced by substituting aspartyl residues in unimproved
PT immunoglobulin E prone to isomerization by other residues by affinity
PT maturation with phage display.
XX
PS Claim 4; Fig 12; 87pp; English.
XX This invention relates to a nucleotide sequence encoding an antibody with
CC improved anti-IgE antibody activity. The antibody has improved action due
CC to a process comprising, a) identifying aspartyl residues prone to
CC isomerisation in unimproved anti-IgE (immunoglobulin E) antibody; b)
CC substituting alternative residues to create candidate molecules, and c)
CC selecting those candidate molecules which display affinity against the
CC target molecule. Use of the antibody results in antiasthmatic;
CC antiasthmatic; ophthalmological; dermatological and antiinflammatory
CC activity. The antibodies are useful for treating IgE-mediated disorders
CC such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and
CC food allergies. The mutant antibodies produced by the above mentioned
CC nucleic acids may also be used as affinity purification agents and in
CC diagnostic assays for detecting the expression of an antigen of interest
CC in specific cell, tissues or serum. Amino acid sequences AAB76936-
CC AAB76960 represent fragments of anti-IgE antibodies of the invention.
CC Polynucleotide sequence AAF69253 represents an expression plasmid used in
CC the course of the invention, and oligonucleotides AAF69254 - AAF69271 are
CC used in the generation of affinity improved anti-IgE antibodies
XX
SQ Sequence 451 AA;

Query Match 97.4%; Score 2369; DB 4; Length 451;
Best Local Similarity 98.0%; Pred. No. 5e-138;
Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

QY 1 EVQLVSGGGLVQPGGSLRLSCAVSGYSITSGYSWNIQAPGKGLEWVASITYDGSTNY 60
Db 1 EVQLVSGGGLVQPGGSLRLSCAVSGYSITSGYSWNIQAPGKGLEWVASIKYGETKY 60
QY 61 ADSVKGRFTISRDDSKNTFYLQWNSLRAEDTAVYYCARGSHYFGHHFAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLQWNSLRAEDTAVYYCARGSHYFGHHFAVWGQGLTVTVS 120

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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:43:38 ; Search time 22.2787 Seconds
(without alignments)
1049.728 Million cell updates/sec

Title: US-09-925-179-8

Perfect score: 2432

Sequence: 1 EVQLVESGGGLVQPGGSLRL.....MHEALHHYTKSLSPGK 453

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2432	100.0	453	3	US-08-466-151-8
2	2432	100.0	453	4	US-08-466-163B-8
3	2432	100.0	453	4	US-09-802-096-8
4	2391	98.3	451	2	US-08-887-352B-14
5	2391	98.3	451	2	US-08-887-352B-16
6	2391	98.3	451	3	US-08-466-151-65
7	2391	98.3	451	3	US-09-109-207C-14
8	2391	98.3	451	3	US-09-109-207C-16
9	2391	98.3	451	3	US-09-296-005-14
10	2391	98.3	451	3	US-09-296-005-16
11	2391	98.3	451	4	US-09-920-171-14
12	2391	98.3	451	4	US-09-920-171-16
13	2369	97.4	451	2	US-08-887-352B-18
14	2369	97.4	451	3	US-09-109-207C-18
15	2369	97.4	451	3	US-09-282-505-2
16	2369	97.4	451	3	US-03-054-255-2
17	2369	97.4	451	3	US-09-296-005-18
18	2369	97.4	451	4	US-09-282-846-2
19	2369	97.4	451	4	US-09-680-145-2
20	2369	97.4	451	4	US-09-920-171-18
21	2214.5	91.1	452	3	US-09-027-449-71
22	2214.5	91.1	452	3	US-09-026-985-71
23	2214.5	91.1	452	4	US-09-121-952A-71
24	2214.5	91.1	452	4	US-09-234-340A-71
25	2179.5	89.6	449	4	US-09-679-397-2
26	2179.5	89.6	449	4	US-09-680-148-2
27	2179.5	89.6	449	4	US-09-304-465A-2

28	2164.5	89.0	459	1	US-08-157-101A-7	Sequence 7, Appli
29	2132	87.7	478	3	US-08-487-550-8	Sequence 8, Appli
30	2132	87.7	478	4	US-09-526-098-8	Sequence 8, Appli
31	2117.5	87.1	473	3	US-09-049-672A-4	Sequence 4, Appli
32	2093	86.1	476	3	US-08-487-550-12	Sequence 12, Appli
33	2093	86.1	476	4	US-09-526-098-12	Sequence 12, Appli
34	2092	86.0	449	1	US-08-458-516-13	Sequence 13, Appli
35	2078	85.4	472	4	US-08-397-411-7	Sequence 7, Appli
36	2073.5	85.3	446	3	US-09-485-737B-67	Sequence 67, Appli
37	2069	85.1	468	4	US-08-487-550-4	Sequence 4, Appli
38	2069	85.1	476	3	US-08-487-550-4	Sequence 4, Appli
39	2069	85.1	476	4	US-09-526-098-4	Sequence 4, Appli
40	2069	85.1	711	4	US-09-485-737B-90	Sequence 90, Appli
41	2056.5	84.6	467	3	US-09-049-672A-8	Sequence 8, Appli
42	2056.5	84.6	475	4	US-09-740-002-27	Sequence 27, Appli
43	2052.5	84.4	467	1	US-08-704-744-81	Sequence 81, Appli
44	2050	84.3	451	4	US-09-472-087-70	Sequence 70, Appli
45	2047	84.2	443	5	PCT-US96-13152-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-466-151-8
; Sequence 8, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: Amino Acid

TOPOLOGY: Linear
US-08-466-151-8
Query Match 100.0%; Score 2432; DB 3; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.1e-184;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
61 ADSVKGRFTISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTS 120
61 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
61 ADSVKGRFTISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTS 120
61 ADSVKGRFTISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTS 120
121 SASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
121 SASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
61 ADSVKGRFTISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTS 120
61 ADSVKGRFTISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTS 120
121 SASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
121 SASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
181 QSSGLYSLSVWTVPPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
181 QSSGLYSLSVWTVPPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
121 SASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
121 SASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
181 QSSGLYSLSVWTVPPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
181 QSSGLYSLSVWTVPPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
301 QYNSTYRVVSVLTVQLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
301 QYNSTYRVVSVLTVQLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 420
361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 420
421 SRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 453
421 SRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 453

RESULT 2
US-08-466-163B-8
; Sequence 8, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mae11, version 1 heavy chain
US-08-466-163B-8
Query Match 100.0%; Score 2432; DB 4; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.1e-184;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60

1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
61 ADSVKGRFTISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTS 120
61 ADSVKGRFTISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTS 120
121 SASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
121 SASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
181 QSSGLYSLSVWTVPPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
181 QSSGLYSLSVWTVPPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
241 LGGPSVFLFPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
241 LGGPSVFLFPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
301 QYNSTYRVVSVLTVQLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
301 QYNSTYRVVSVLTVQLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 420
361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 420
421 SRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 453
421 SRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 453

RESULT 3
US-09-802-096-8
; Sequence 8, Application US/09802096
; Patent No. 6685939
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mae11, version 1 heavy chain
US-09-802-096-8
Query Match 100.0%; Score 2432; DB 4; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.1e-184;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
61 ADSVKGRFTISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTS 120
61 ADSVKGRFTISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTS 120

QY 121 SASTKKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 180
Db 121 SASTKKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 180
QY 181 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 240
Db 181 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 240
QY 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
QY 301 QYNSTYRVVSVLTVQLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db 301 QYNSTYRVVSVLTVQLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
Db 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
QY 421 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453
Db 421 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453

RESULT 4
US-08-887-352B-14
; Sequence 14, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-14

Query Match 98.3%; Score 2391; DB 2; Length 451;
Best Local Similarity 98.9%; Pred. No. 3.6e-181;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNIQAPGKGLEWVASITYDGSNTY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNIQAPGKGLEWVASITYDGSNTY 60

QY 61 ADSVKGRFTISRDDSKNTFYLQWNSLRAEDTAVYYCARGSHYFGHWHFAVMGQGLTVTS 120
Db 61 NPSVKGRITISRDDSKNTFYLQWNSLRAEDTAVYYCARGSHYFGHWHFAVMGQGLTVTS 120
QY 121 SASTKKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 238
QY 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY 301 QYNSTYRVVSVLTVQLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db 299 QYNSTYRVVSVLTVQLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451

RESULT 5
US-08-887-352B-16
; Sequence 16, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-16

Query Match 98.3%; Score 2391; DB 2; Length 451;
Best Local Similarity 98.9%; Pred. No. 3.6e-181;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNIQAPGKGLEWVASITYDGSNTY 60

Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKGLEWVASITYDGSNTY 60
QY 61 ADSVKGRFTISRDDSKNTFYIQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYIQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120
QY 121 SASTKKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPPCPAPEL 240
Db 179 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPPCPAPEL 238
QY 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDDEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDDEVKFNWYVDGVEVHNAKTKPREE 298
QY 301 QYNSTYRVVSVLTVQLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 360
Db 299 QYNSTYRVVSVLTVQLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQGNVVFSCVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQGNVVFSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 6
US-08-466-151-65
; Sequence 65, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.

; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-65

Query Match 98.3%; Score 2391; DB 3; Length 451;
Best Local Similarity 98.9%; Pred. No. 3.6e-181;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKGLEWVASITYDGSNTY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKGLEWVASITYDGSNTY 60

QY 61 ADSVKGRFTISRDDSKNTFYIQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYIQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120

QY 121 SASTKKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 178

QY 181 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPPCPAPEL 240
Db 179 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPPCPAPEL 238

QY 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDDEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDDEVKFNWYVDGVEVHNAKTKPREE 298

QY 301 QYNSTYRVVSVLTVQLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 360
Db 299 QYNSTYRVVSVLTVQLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 358

QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418

QY 421 SRWQGNVVFSCVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQGNVVFSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 7
US-09-109-207C-14
; Sequence 14, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptid
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-14

Query Match 98.3%; Score 2391; DB 3; Length 451;

Best Local Similarity 98.9%; Pred. No. 3.6e-181;	
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;	
Qy	1 EVQLVESGGCLVQPGGSLRLSCA
Db	1 EVQLVESGGCLVQPGGSLRLSCA
Qy	61 ADSVKGRFTISRDDSKNTFYLOM
Db	61 NPSVKGRITISRDDSKNTFYLOM
Qy	121 SASTKGPSVFPELAPSSKSTSG
Db	121 SAST--KGPSVFPELAPSSKST
Qy	181 QSSGLYSLSSVTVPPSSSLGTQY
Db	179 QSSGLYSLSSVTVPPSSSLGTQY
Qy	241 LGGPSVFLFPPKPKDTLMISRTPE
Db	239 LGGPSVFLFPPKPKDTLMISRTPE
Qy	301 QYNSTYRVVSVLTVLIHQDWLNG
Db	299 QYNSTYRVVSVLTVLIHQDWLNG
Qy	361 REEMTKNQVSLTCLVKGFYPSDIA
Db	359 REEMTKNQVSLTCLVKGFYPSDIA
Qy	421 SRWQQGNVFSCSVMHEALHNHYT
Db	419 SRWQQGNVFSCSVMHEALHNHYT

RESULT 8
 US-09-109-207C-16
 ; Sequence 16, Application US/09109207C
 ; Patent No. 6172213
 ; GENERAL INFORMATION:
 ; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe
 ; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
 ; FILE REFERENCE: P1123R1
 ; CURRENT APPLICATION NUMBER: US/09/109,207C
 ; CURRENT FILING DATE: 1998-06-30
 ; PRIOR APPLICATION NUMBER: US 60/051,554
 ; PRIOR FILING DATE: 1997-07-03
 ; NUMBER OF SEQ ID NOS: 44
 ; SEQ ID NO 16
 ; LENGTH: 451
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; NAME/KEY: Artificial
 ; LOCATION: 1-451
 ; OTHER INFORMATION: Heavy chain sequence derived from MAE11
 US-09-109-207C-16

Query Match	98.3%;	Score 2391;	DB 3;	Length 451;
Best Local Similarity	98.9%;	Pred. No. 3.6e-181;		
Matches 448;	Conservative	0;	Mismatches 3;	Indels 2;
			Gaps	1;

QY	1	EVQLVESGGGLVQPGGSLRLS	CAVSGYSITSGYSMNWIRQAPKGLEWVASITYDGS	TNY	60
DB	1	EVQLVESGGGLVQPGGSLRLS	CAVSGYSITSGYSMNWIRQAPKGLEWVASITYDGS	TNY	60
QY	61	ADSVKGRFTISRDDSKNTFYLQMN	SLRAEDTAVYYCARGSHYFGHW	HFAVWGQGLVT	VS
DB	61	NPSVKGRITISRDDSKNTFYLQMN	SLRAEDTAVYYCARGSHYFGHW	HFAVWGQGLVT	VS
QY	121	SASTKGKGPSVFPPLAPSKSTSGG	TAAALGCLVKDYFPEPTVSWNSG	ALTSGVHTTFAVL	180

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Db      121  SAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178
QY      181  QSSGLYSLSSWVTVFPSSSLGTQTYICNVNHHKPSNTKVDDKKVEPKSCDKTHCTCPPCPAPEL 240
Db      179  QSSGLYSLSSWVTVFPSSSLGTQTYICNVNHHKPSNTKVDDKKVEPKSCDKTHCTCPPCPAPEL 238
QY      241  LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db      239  LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY      301  QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db      299  QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY      361  REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420
Db      359  REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
QY      421  SRWQGNVFPSCSVMHREALHNHYTQKSLSLSPGK 453
Db      419  SRWQGNVFPSCSVMHREALHNHYTQKSLSLSPGK 451

RESULT 9
US-09-296-005-14
; Sequence 14, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-14

```

	Query Match	98.3%;	Score 2391;	DB 3;	Length 451;
	Best Local Similarity	98.9%;	Pred. No. 3.6e-181;		
	Matches 448;	Conservative 0;	Mismatches 3;	Indels 2;	Gaps 1;
QY	1	EVQLVESGGGLVQPGGSLRLS	CAVSGYSITSGYSMNWIR	QAPGKGLEWVASITYDGS	TNY 60
DB	1	EVQLVESGGGLVQPGGSLRLS	CAVSGYSITSGYSMNWIR	QAPGKGLEWVASITYDGS	TNY 60
QY	61	ADSVKGRFTISRDDSKNTFYLQMN	SLRAEDTAVVYCARGSHYFGHWHF	AVWGQGLTVTS	120
DB	61	NPSVKGRITISRDDSKNTFYLQMN	SLRAEDTAVVYCARGSHYFGHWHF	AVWGQGLTVTS	120
QY	121	SASTKGKGPSVFPPLAPSSKSTSGG	TAAALGCLVKDYFPEPVTVSWNSG	ALTSGVHTFPAVL	180
DB	121	SAST--KGPSVFPPLAPSSKSTSGG	TAAALGCLVKDYFPEPVTVSWNSG	ALTSGVHTFPAVL	178
QY	181	QSSGLYSLSVVTVPSSSLGTQTYI	CNVNHKPSNTKVDKKVEPKSCD	KTHTCPCPAPEL	240
DB	179	QSSGLYSLSVVTVPSSSLGTQTYI	CNVNHKPSNTKVDKKVEPKSCD	KTHTCPCPAPEL	238
QY	241	LGGPSVFLPFPKPKDTLMISRTPE	VTCTVVVDVSHEDPEVKENWYVDG	VEVHNAKTKPREE	300
DB	239	LGGPSVFLPFPKPKDTLMISRTPE	VTCTVVVDVSHEDPEVKENWYVDG	VEVHNAKTKPREE	298
QY	301	QYNSTYRVVSVLTVTLHQDWLNGK	EYKCKVSNKALPAPIEKTISKAKG	QPREPQVYTLPPS	360
DB	299	QYNSTYRVVSVLTVTLHQDWLNGK	EYKCKVSNKALPAPIEKTISKAKG	QPREPQVYTLPPS	358

QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 10
US-09-296-005-16
; Sequence 16, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-16

Query Match 98.3%; Score 2391; DB 3; Length 451;
Best Local Similarity 98.9%; Pred. No. 3.6e-181;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSNTY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSNTY 60
QY 61 ADSVKGRFTISRDDSKNTFYLQMNSLRAEDTAVYVCARGSHYFGHWHFVAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYVCARGSHYFGHWHFVAVWGQGLTVTVS 120
QY 121 SASTKGKPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSVWTVPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSVWTVPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSCDKTHTCPPCPAPEL 238
QY 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY 301 QYNSTYRVVSVLTVQLHQLDNLNGKEYCKKVSNAKALPAIEKTIISKAKGQPREPOVYTLPPS 360
Db 299 QYNSTYRVVSVLTVQLHQLDNLNGKEYCKKVSNAKALPAIEKTIISKAKGQPREPOVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 11
US-09-920-171-14
; Sequence 14, Application US/09920171

; Patent No. 6682735
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-14

Query Match 98.3%; Score 2391; DB 4; Length 451;
Best Local Similarity 98.9%; Pred. No. 3.6e-181;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSNTY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSNTY 60
QY 61 ADSVKGRFTISRDDSKNTFYLQMNSLRAEDTAVYVCARGSHYFGHWHFVAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYVCARGSHYFGHWHFVAVWGQGLTVTVS 120
QY 121 SASTKGKPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSVWTVPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSVWTVPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSCDKTHTCPPCPAPEL 238
QY 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY 301 QYNSTYRVVSVLTVQLHQLDNLNGKEYCKKVSNAKALPAIEKTIISKAKGQPREPOVYTLPPS 360
Db 299 QYNSTYRVVSVLTVQLHQLDNLNGKEYCKKVSNAKALPAIEKTIISKAKGQPREPOVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 12
US-09-920-171-16
; Sequence 16, Application US/09920171
; Patent No. 6682735
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01

RESULT 14
US-09-109-207C-18
; Sequence 18, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta,
; TITLE OF INVENTION: Improved Anti-IgE Antibodies
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 18
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451

OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-18

Query Match 97.4%; Score 2369; DB 3; Length 451;
Best Local Similarity 98.0%; Pred. No. 2e-179;
Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

Qy	1	EVQLVESGGGLVQPGGSLRLS	CAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY	60
Db	1	EVQLVESGGGLVQPGGSLRLS	CAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETKY	60
Qy	61	ADSVKGRFTISRDDSKNTFY	LQMNSLRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTVS	120
Db	61	NPSVKGRITISRDDSKNTFY	LQMNSLRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTVS	120
Qy	121	SASTKGKPSVFPPLAPSSK	STSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL	180
Db	121	SAST--KGPSVFPPLAPSSK	STSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL	178
Qy	181	QSSGLYSLSSVTVPSSSLG	TQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPEL	240
Db	179	QSSGLYSLSSVTVPSSSLG	TQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPEL	238
Qy	241	LGGSVFLFPPKPKDTLMIS	RTPETVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE	300
Db	239	LGGSVFLFPPKPKDTLMIS	RTPETVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE	298
Qy	301	QYNSTYRVVSVLTVHLHQD	WLNKKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS	360
Db	299	QYNSTYRVVSVLTVHLHQD	WLNKKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS	358
Qy	361	REEMTKNQVSLTCLVKGF	YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK	420
Db	359	REEMTKNQVSLTCLVKGF	YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK	418
Qy	421	SRWQOGNVFSCSVMEALH	NHYTQKSLSLSPGK 453	
Db	419	SRWQOGNVFSCSVMEALH	NHYTQKSLSLSPGK 451	

RESULT 15
US-09-282-505-2
; Sequence 2, Application US/09282505A
; Patent No. 6194551
; GENERAL INFORMATION:
; APPLICANT: Esche Bkinaduese Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R1
; CURRENT APPLICATION NUMBER: US/09/282,505A
; CURRENT FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-451
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6194551
US-09-282-505-2

Query Match 97.4%; Score 2369; DB 3; Length 451;
Best Local Similarity 98.0%; Pred. No. 2e-179;
Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

Qy	1	EVQLVESGGGLVQPGGSLRLS	CAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY	60
Db	1	EVQLVESGGGLVQPGGSLRLS	CAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETKY	60
Qy	61	ADSVKGRFTISRDDSKNTFY	LQMNSLRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTVS	120
Db	61	NPSVKGRITISRDDSKNTFY	LQMNSLRAEDTAVYICARGSHYFGHWHFAVWGQGLTVTVS	120

Qy	121	SASTKGKPSVFPPLAPSSK	STSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL	180
Db	121	SAST--KGPSVFPPLAPSSK	STSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL	178
Qy	181	QSSGLYSLSSVTVPSSSLG	TQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPEL	240
Db	179	QSSGLYSLSSVTVPSSSLG	TQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPEL	238
Qy	241	LGGSVFLFPPKPKDTLMIS	RTPETVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE	300
Db	239	LGGSVFLFPPKPKDTLMIS	RTPETVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE	298
Qy	301	QYNSTYRVVSVLTVHLHQD	WLNKKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS	360
Db	299	QYNSTYRVVSVLTVHLHQD	WLNKKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS	358
Qy	361	REEMTKNQVSLTCLVKGF	YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK	420
Db	359	REEMTKNQVSLTCLVKGF	YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK	418
Qy	421	SRWQOGNVFSCSVMEALH	NHYTQKSLSLSPGK 453	
Db	419	SRWQOGNVFSCSVMEALH	NHYTQKSLSLSPGK 451	

Search completed: May 13, 2004, 15:48:47
Job time : 23.2787 secs

QY 61 ADSVKGRFTISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120
Db 61 ADSVKGRFTISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120
QY 121 SASTKGKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 180
Db 121 SASTKGKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 180
QY 181 QSSGLYSLSSVWTVPPSSSLGTQTYICNVNHPKPSNTKVDKKEPKSCDKTHTCTCPAPAPL 240
Db 181 QSSGLYSLSSVWTVPPSSSLGTQTYICNVNHPKPSNTKVDKKEPKSCDKTHTCTCPAPAPL 240
QY 241 LGGPSVFLFPPKPKDTLMSRTPEVTCVAVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 241 LGGPSVFLFPPKPKDTLMSRTPEVTCVAVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPS 360
Db 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPS 360
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
Db 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
QY 421 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453
Db 421 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453

RESULT 2

US-09-802-096-8
; Sequence 8, Application US/09802096
; Patent No. US20010038839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mae11, version 1 heavy chain
US-09-802-096-8

Query Match 100.0%; Score 2432; DB 9; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.1e-159;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
QY 61 ADSVKGRFTISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120
Db 61 ADSVKGRFTISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120
QY 121 SASTKGKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 180

Db 121 SASTKGKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 180
QY 181 QSSGLYSLSSVWTVPPSSSLGTQTYICNVNHPKPSNTKVDKKEPKSCDKTHTCTCPAPAPL 240
Db 181 QSSGLYSLSSVWTVPPSSSLGTQTYICNVNHPKPSNTKVDKKEPKSCDKTHTCTCPAPAPL 240
QY 241 LGGPSVFLFPPKPKDTLMSRTPEVTCVAVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 241 LGGPSVFLFPPKPKDTLMSRTPEVTCVAVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPS 360
Db 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPS 360
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
Db 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
QY 421 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453
Db 421 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453

RESULT 3

US-09-925-179-8
; Sequence 8, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IGE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mae11, version 1 heavy chain
US-09-925-179-8

Query Match 100.0%; Score 2432; DB 10; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.1e-159;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
QY 61 ADSVKGRFTISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120
Db 61 ADSVKGRFTISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120
QY 121 SASTKGKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 180
Db 121 SASTKGKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 180
QY 181 QSSGLYSLSSVWTVPPSSSLGTQTYICNVNHPKPSNTKVDKKEPKSCDKTHTCTCPAPAPL 240

Db 181 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPCPAPEL 240
Qy 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREE 300
Db 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREE 300
Qy 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Qy 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDK 420
Db 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDK 420
Qy 421 SRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 453
Db 421 SRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 453

RESULT 4

US-09-920-171-14
; Sequence 14, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-14

Query Match 98.3%; Score 2391; DB 9; Length 451;
Best Local Similarity 98.9%; Pred. No. 7.3e-157;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSNTY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSNTY 60
Qy 61 ADSVKGRFTISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHHFVAVWGQGLVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHHFVAVWGQGLVTVS 120
Qy 121 SASTKGKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178
Qy 181 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPCPAPEL 240
Db 179 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPCPAPEL 238
Qy 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREE 300
Db 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREE 298
Qy 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358

Qy 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDK 418
Qy 421 SRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 5

US-09-920-171-16
; Sequence 16, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-16

Query Match 98.3%; Score 2391; DB 9; Length 451;
Best Local Similarity 98.9%; Pred. No. 7.3e-157;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSNTY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSNTY 60
Qy 61 ADSVKGRFTISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHHFVAVWGQGLVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHHFVAVWGQGLVTVS 120
Qy 121 SASTKGKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178
Qy 181 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPCPAPEL 240
Db 179 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPCPAPEL 238
Qy 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREE 300
Db 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREE 298
Qy 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
Qy 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDK 418
Qy 421 SRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 6

US-09-925-179-65
; Sequence 65, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 65
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)8b of Tab1
US-09-925-179-65

Query Match 98.3%; Score 2391; DB 10; Length 451;
Best Local Similarity 98.9%; Pred. No. 7.3e-157;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPGKGLEWVASITYDGSTNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPGKGLEWVASITYDGSTNY 60
QY 61 ADSVKGRFTISRDDSKNTFYLQMSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLQMSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120
QY 121 SASTKGKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSVWTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPEL 240
Db 179 QSSGLYSLSVWTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPEL 238
QY 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKFNWYVDGVEVHNATKPREE 300
Db 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKFNWYVDGVEVHNATKPREE 298
QY 301 QYNSTYRVVSVLTVQLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db 299 QYNSTYRVVSVLTVQLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK 453
Db 419 SRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK 451

RESULT 7
US-10-113-996-14
; Sequence 14, Application US/10113996
; Publication No. US20030149244A1
; GENERAL INFORMATION:

; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies
; FILE REFERENCE: P1123C3US
; CURRENT APPLICATION NUMBER: US/10/113,996
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 09/920,171
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-10-113-996-14

Query Match 98.3%; Score 2391; DB 14; Length 451;
Best Local Similarity 98.9%; Pred. No. 7.3e-157;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPGKGLEWVASITYDGSTNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPGKGLEWVASITYDGSTNY 60
QY 61 ADSVKGRFTISRDDSKNTFYLQMSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLQMSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120
QY 121 SASTKGKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSVWTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPEL 240
Db 179 QSSGLYSLSVWTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPEL 238
QY 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKFNWYVDGVEVHNATKPREE 300
Db 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKFNWYVDGVEVHNATKPREE 298
QY 301 QYNSTYRVVSVLTVQLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db 299 QYNSTYRVVSVLTVQLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK 453
Db 419 SRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK 451

RESULT 8
US-10-113-996-16
; Sequence 16, Application US/10113996
; Publication No. US20030149244A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies
; FILE REFERENCE: P1123C3US
; CURRENT APPLICATION NUMBER: US/10/113,996
; CURRENT FILING DATE: 2002-04-01

LENGTH: 451
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)9 of Table US-09-925-179-68

Query Match 97.8%; Score 2379; DB 10; Length 451;
Best Local Similarity 97.8%; Pred. No. 4.9e-156;
Matches 443; Conservative 4; Mismatches 4; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPGKLEWVASITYDGSNTY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPGKLEWVASITYDGSNTY 60
QY 61 ADSVKGRFTISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120
QY 121 SASTKGKPSVFPPLAPSSKSTSGTAAALGCLVCKDYFPEPVTVSNWNGALTSVHTFPAVL 180
Db 121 SAST--KGPSVFPPLAPSSKSTSGTAAALGCLVCKDYFPEPVTVSNWNGALTSVHTFPAVL 178
QY 181 QSSGLYSLSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 238
QY 241 LGGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY 301 QYNSTYRVVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPS 360
Db 299 QYNSTYRVVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQQGNVFSCVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQQGNVFSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 11
US-09-920-171-18
Sequence 18, Application US/09920171
Patent No. US20020054878A1
GENERAL INFORMATION:
APPLICANT: Lowman, Henry B.
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
APPLICANT: Lowe, John
TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
FILE REFERENCE: P1123C2US
CURRENT APPLICATION NUMBER: US/09/920.171
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: US 08/887,352
PRIOR FILING DATE: 1997-07-02
PRIOR APPLICATION NUMBER: US 09/296,005
PRIOR FILING DATE: 1999-04-21
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 18
LENGTH: 451
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Heavy chain sequence derived from MAb11
US-09-920-171-18

Query Match 97.4%; Score 2369; DB 9; Length 451;
Best Local Similarity 98.0%; Pred. No. 2.4e-155;
Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPGKLEWVASITYDGSNTY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPGKLEWVASIKYSGETKY 60
QY 61 ADSVKGRFTISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120
QY 121 SASTKGKPSVFPPLAPSSKSTSGTAAALGCLVCKDYFPEPVTVSNWNGALTSVHTFPAVL 180
Db 121 SAST--KGPSVFPPLAPSSKSTSGTAAALGCLVCKDYFPEPVTVSNWNGALTSVHTFPAVL 178
QY 181 QSSGLYSLSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 238
QY 241 LGGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY 301 QYNSTYRVVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPS 360
Db 299 QYNSTYRVVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQQGNVFSCVMHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQQGNVFSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 12
US-09-792-938-2
Sequence 2, Application US/09792938
Publication No. US20030166868A1
GENERAL INFORMATION:
APPLICANT: Esohe Ekinaduese Idusogie et al.
TITLE OF INVENTION: Polypeptide Variants
FILE REFERENCE: P1266R1
CURRENT APPLICATION NUMBER: US/09/792,938
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 09/282,505
PRIOR FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
LENGTH: 451
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: Artificial Sequence
LOCATION: 1-451
OTHER INFORMATION: Sequence is completely synthesized
US-09-792-938-2

Query Match 97.4%; Score 2369; DB 10; Length 451;
Best Local Similarity 98.0%; Pred. No. 2.4e-155;
Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPGKLEWVASITYDGSNTY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPGKLEWVASIKYSGETKY 60
QY 61 ADSVKGRFTISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120
QY 121 SASTKGKPSVFPPLAPSSKSTSGTAAALGCLVCKDYFPEPVTVSNWNGALTSVHTFPAVL 180
Db 121 SAST--KGPSVFPPLAPSSKSTSGTAAALGCLVCKDYFPEPVTVSNWNGALTSVHTFPAVL 178

QY 181 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238
QY 241 LGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQQGNVFSCSVNHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQQGNVFSCSVNHEALHNHYTQKSLSLSPGK 451

RESULT 13

US-10-113-996-18
; Sequence 18, Application US/10113996
; Publication No. US20030149244A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-Ige Antibodies
; FILE REFERENCE: P1123C3US
; CURRENT APPLICATION NUMBER: US/10/113,996
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 09/920,171
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 18
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-10-113-996-18

Query Match 97.4%; Score 2369; DB 14; Length 451;
Best Local Similarity 98.0%; Pred. No. 2.4e-155;
Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETKY 60
QY 61 ADSVKGRFTISRDDSKNTFYLQMNLSRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLQMNLSRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120
QY 121 SASTKGKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238
QY 241 LGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQQGNVFSCSVNHEALHNHYTQKSLSLSPGK 453
Db 239 LGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQQGNVFSCSVNHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQQGNVFSCSVNHEALHNHYTQKSLSLSPGK 451

RESULT 14

US-10-292-869-2
; Sequence 2, Application US/10292869
; Publication No. US20030158389A1
; GENERAL INFORMATION:
; APPLICANT: Esche Ekinaduese Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R2
; CURRENT APPLICATION NUMBER: US/10/292,869
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US/09/282,846
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-451
; OTHER INFORMATION: Sequence is completely synthesized
US-10-292-869-2

Query Match 97.4%; Score 2369; DB 14; Length 451;
Best Local Similarity 98.0%; Pred. No. 2.4e-155;
Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETKY 60
QY 61 ADSVKGRFTISRDDSKNTFYLQMNLSRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLQMNLSRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120
QY 121 SASTKGKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238
QY 241 LGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQQGNVFSCSVNHEALHNHYTQKSLSLSPGK 453
Db 419 SRWQQGNVFSCSVNHEALHNHYTQKSLSLSPGK 451

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:38:23 ; Search time 18.9031 Seconds
(without alignments)
2305.161 Million cell updates/sec

Title: US-09-925-179-8
Perfect score: 2432
Sequence: 1 EVQLVESGGGLVQPGGSLRL.....MHEALHNHYTQKSLSLSPGK 453

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: Pirl:*
2: Pirl2:*
3: Pirl3:*
4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1750	72.0	330	1	GHU	Ig gamma-1 chain C
2	1625.5	66.8	377	2	A23511	Ig gamma-3 chain C
3	1623.5	66.8	377	2	A60764	Ig gamma-3 chain C
4	1599	65.7	326	1	G2HU	Ig gamma-2 chain C
5	1585.5	65.2	327	1	G4HU	Ig gamma-4 chain C
6	1507.5	62.0	444	2	PC4436	monoclonal antibod
7	1477	60.7	374	2	S69339	Ig heavy chain V r
8	1467	60.3	470	2	S22080	Ig heavy chain pre
9	1444	59.4	472	2	S31459	Ig gamma-1 chain -
10	1403.5	57.7	469	2	S37483	Ig gamma-2a chain
11	1403	57.7	446	2	S40295	Ig gamma-2a chain
12	1359	55.9	474	1	G2MS11	Ig gamma-2b chain
13	1345.5	55.3	475	2	S01321	Ig gamma-2a chain
14	1263	51.9	328	2	I47159	Ig gamma-2a chain
15	1257	51.7	328	2	I47160	Ig gamma-2b chain
16	1254	51.6	255	4	S31866	Ig gamma-1 chain C
17	1248	51.3	234	2	PT0207	Ig gamma chain C r
18	1231.5	50.6	323	1	GHRB	Ig gamma chain C r
19	1231	50.6	328	2	I47158	Ig gamma 1 chain c
20	1227	50.5	328	2	I47161	Ig gamma 3 chain c
21	1202.5	49.4	329	1	G2GP	Ig gamma-2 chain C
22	1162.5	47.8	308	2	C30554	Ig heavy chain C r
23	1157	47.6	289	1	G3HUWI	Ig gamma-3 heavy c
24	1150	47.3	326	2	PS0017	Ig gamma-1 chain C
25	1142	47.0	324	1	G1MS	Ig gamma-1 chain C
26	1142	47.0	329	1	G3MSC	Ig gamma-3 chain C
27	1139.5	46.9	333	2	S0018	Ig gamma-2b chain
28	1137	46.8	393	1	G1MSM	Ig gamma-1 chain C
29	1131	46.5	398	1	G3MSM	Ig gamma-3 chain C

Ig gamma-2a chain
Ig gamma-2a chain
Ig gamma-2a chain
Ig gamma-2c chain
Ig gamma-2a chain
Ig gamma-2 chain C
Ig gamma-2b chain
Ig gamma 4 chain C
Ig epsilon chain C
Ig heavy chain VHI
Ig heavy chain pre
Ig gamma-1 heavy c
Ig Y heavy chain (
Ig heavy chain V-I
Ig heavy chain (DO
Ig mu chain precur

ALIGNMENTS

RESULT 1

GHU
Ig gamma-1 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 16-Jul-1999
C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A;Reference number: A93433; MUID:82274238; PMID:6287432
A;Accession: A93433
A;Molecule type: DNA
A;Residues: 1-330 <ELL>
A;Cross-references: EMBL:Z17370
A;Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,
A;Note: Lys-330 is removed after translation
R;Harris, L.J.
submitted to the EMBL Data Library, October 1992
A;Reference number: S33904
A;Accession: S36861
A;Molecule type: DNA
A;Residues: 2-330 <HAR>
A;Cross-references: EMBL:Z17370
R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A;Reference number: S33887; MUID:83001943; PMID:6811139
A;Accession: S33887
A;Molecule type: DNA
A;Residues: 88-113;235-330 <TAK>
A;Cross-references: EMBL:Z17370
R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seque
A;Reference number: A90563; MUID:71064024; PMID:5489771
A;Contents: myeloma protein Eu
A;Accession: B90563
A;Molecule type: protein
A;Residues: 1-96,'R',98-135 <CUN>
A;Note: this sequence has the G1m(3) marker, 97-Arg
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequ
A;Reference number: A90564; MUID:71064025; PMID:5530842
A;Contents: Eu
A;Accession: A90564
A;Molecule type: protein
A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240
A;Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met
R;Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie)

igen Primaerstruktur.
A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
A;Molecule type: protein
A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A;Note: this sequence has the G1m(17) and G1m(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KO1
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KOL; disulfide bonds
A;Accession: A91723
A;Molecule type: protein
A;Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
A;Note: this sequence has the G1m(3) and G1m(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 72.0%; Score 1750; DB 1; Length 330;
Best Local Similarity 98.8%; Pred. No. 8.3e-95;
Matches 328; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY 122 ASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 181
Db 1 AST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 58

QY 182 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 241
Db 59 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 118

QY 242 GGPSVFLFPPKPKDITLMSRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 301
Db 119 GGPSVFLFPPKPKDITLMSRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 178

QY 302 YNSTYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSR 361
Db 179 YNSTYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSR 238

QY 362 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGSFFLYSKLTVDKS 421
Db 239 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGSFFLYSKLTVDKS 298

QY 422 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453
Db 299 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330

RESULT 2
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: c
A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Accession: A23511
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: GB:X03604; GB:M12958; NID:933070; PIDN:CAA27268.1; PID:G577056
C;Genetics:
A;Gene: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 66.8%; Score 1625.5; DB 2; Length 377;
Best Local Similarity 82.1%; Pred. No. 1.7e-87;
Matches 311; Conservative 8; Mismatches 11; Indels 49; Gaps 2;

QY 122 ASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 181
Db 1 AST--KGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 58

QY 182 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV----- 221
Db 59 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVELKTPLGDTTHTCPRCPPEPK 118

QY 222 -----EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK 254
Db 119 SCDTPPPCPCPEPKSCDTPPPCPCPEPKSCDTPPPCPCPEPKSCDTPPPCPCPEPK 178

QY 255 DTLMSRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVSLTV 314
Db 179 DTLMSRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVSLTV 238

QY 315 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCL 374
Db 239 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCL 298

QY 375 VKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGSFFLYSKLTVDKSRWQQGNVFCFSVM 434
Db 299 VKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGSFFLYSKLTVDKSRWQQGNVFCFSVM 358

QY 435 HEALHNHYTQKSLSLSPGK 453
Db 359 HEALHNRYFTQKSLSLSPGK 377

RESULT 3
A60764
Ig gamma-3 chain C region, form LAT - human
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 conver
A;Reference number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 66.8%; Score 1623.5; DB 2; Length 377;
Best Local Similarity 82.1%; Pred. No. 2.2e-87;
Matches 311; Conservative 8; Mismatches 11; Indels 49; Gaps 2;

QY 122 ASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 181
Db 1 AST--KGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 58

QY 182 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVKDKV----- 221
Db 59 SSGLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVKDKVELKTPGLDTHTCPCRCPEPK 118

QY 222 -----EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKPK 254
Db 119 SCDTPPCPCRCPEPKSCDTPPPCPCRCPEPKSCDTPPPCPCRCPEPKSCDTPPPCPCRCPEPK 178

QY 255 DTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV 314
Db 179 DTLMSRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTV 238

QY 315 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL 374
Db 239 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL 298

QY 375 VKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCFSVM 434
Db 299 VKGFYPSDIAVEWESGQPENNYNTTPPVLDSDGSFFLYSLRLTVDKSRWQEGNVFCFSVM 358

QY 435 HEALHNHYTQKSLSLSPGK 453
Db 359 HEALHNRTQKSLSLSPGK 377

RESULT 4
G2HU
Ig gamma-2 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 21-Jul-2000
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
A;Molecule type: DNA
A;Residues: 1-326 <ELL>
A;Cross-references: GB:J00230; NID:G32759; PIDN:CAB58438.1; PID:G6066056
A;Note: Lys-326 is probably removed posttranslationally
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein Til
A;Accession: A92809
A;Molecule type: protein
A;Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>
A;Note: Trp-156 is at or near the complement-binding site
R;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chain constant region domains of a
A;Reference number: A90752; MUID:80001357; PMID:113060
A;Contents: myeloma protein Zie
A;Accession: A90752
A;Molecule type: protein
A;Residues: 1-24,'E',26-57,'EV',60-85,'132-171','ZZZ',175,'B',177-193,'D',195-196,'Q',198-
A;Note: this sequence has since been revised
R;Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A;Reference number: A93132; MUID:80114419; PMID:118920
A;Contents: Zie
A;Accession: A93132

A;Molecule type: protein
A;Residues: 238-275 <HOF>
R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidat
ned
R;Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:69064124; PMID:5782707
A;Contents: annotation; Sa, disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG2
A;Cross-references: GDB:119338; OMIM:147110
A;Map position: 14q32.33-14q32.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kε
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into]
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;133-202/Domain: immunoglobulin homology <IM2>
F;239-306/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,140-200,246-304/Disulfide bonds: #status experimental
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 65.7%; Score 1599; DB 1; Length 326;
Best Local Similarity 91.3%; Pred. No. 4.9e-86;
Matches 303; Conservative 10; Mismatches 13; Indels 6; Gaps 3;

QY 122 ASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 181
Db 1 AST--KGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 58

QY 182 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKEPKSCDKTHTCPPCPAPELL 241
Db 59 SSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTKVERKCCVE--CPPCPAPP-V 114

QY 242 GGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPREEQ 301
Db 115 AGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTPREEQ 174

QY 302 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 361
Db 175 FNSTFRVVSVLTTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSR 234

QY 362 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSLKLTVDKS 421
Db 235 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPMLDSDGSFFLYSLKLTVDKS 294

QY 422 RWQOGNVFSCSVMHAEALHNHYTQKSLSLSPGK 453
Db 295 RWQOGNVFSCSVMHAEALHNHYTQKSLSLSPGK 326

RESULT 5
G4HU
Ig gamma-4 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 16-Jul-1999
C;Accession: A90933; A90249; A02150
R;Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A;Reference number: A90933; MUID:83157104; PMID:6299662

A;Accession: A90933
A;Molecule type: DNA
A;Residues: 1-327 <ELL>
A;Note: the sequence was determined from the germline gene
R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant
A;Reference number: A90249; MUID:70207560; PMID:4192699
A;Accession: A90249
A;Molecule type: protein
A;Residues: 1-30;81-326 <PIN>
C;Genetics:
A;Gene: GDB:IGHG4
A;Cross-references: GDB:119340; OMIM:147130
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;99-110/Region: hinge
F;134-203/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,141-201,247-305/Disulfide bonds: #status predicted
F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 65.2%; Score 1585.5; DB 1; Length 327;
Best Local Similarity 91.0%; Pred. No. 3e-85;
Matches 302; Conservative 10; Mismatches 15; Indels 5; Gaps 2;

QY 122 ASTKGKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 181
Db 1 AST--KGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 58

QY 182 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTPKVDKKVEPKSCDKTHTCPPCPAPELL 241
Db 59 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTPKVDKRVESK--YGPPCPSCPAPPEFL 115

QY 242 GGPSVFLPFPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 301
Db 116 GGPSVFLPFPKPKDILMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQ 175

QY 302 YNSTYRVSVSLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 361
Db 176 FNSTYRVSVSLTVLHODWLNKGEYCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQ 235

QY 362 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGGSFFLYSKLTVDKS 421
Db 236 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGGSFFLYSRLTVDKS 295

QY 422 RWQGNVFSVCSVMHEALHNHYTQKSLSLSPGK 453
Db 296 RWQGNVFSVCSVMHEALHNHYTQKSLSLSPGK 327

RESULT 6
PC4436
monoclonal antibody 13-1 heavy chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C;Accession: PC4436
R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphy
A;Reference number: JC5810; MUID:98063277; PMID:9398605
A;Accession: PC4436
A;Molecule type: protein
A;Residues: 1-444 <AKA>
C;Comment: This catalytic antibody has peroxidase oxidase activity. It is directed again
C;Superfamily: immunoglobulin C region; immunoglobulin homology

F;251-320/Domain: immunoglobulin homology <IMM>
F;22/Disulfide bonds: interchain (to 98) #status predicted
F;99/Disulfide bonds: interchain (to 109) #status predicted

Query Match 62.0%; Score 1507.5; DB 2; Length 444;
Best Local Similarity 61.7%; Pred. No. 1.4e-80;
Matches 284; Conservative 67; Mismatches 86; Indels 23; Gaps 9;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWMNIRQAPGKLEWVASITYDG---S 57
Db 1 EVQXVETGGGLVLRPGNSLKLSCITSGFTF--SNYRMEHLWLRQPPGKRLEWIAVITKSDNYG 59

QY 58 TNYADSVKGRFTISRDDSKNTFYLQMNSLRRAEDTAVYICARGSHYFGHWHFV--WGQGT 115
Db 60 AKYAESVGRFTISRDDSKSVYLQMNRLREEDTATYICRTP-----WVYAMDCWGQGT 114

QY 116 LVTSSASTKKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 175
Db 115 SVIVSSAKT--TPPSVYPLAPGSAATNSMTVLGCLVKGFPEPVTVTWSGSLSSGVHT 172

QY 176 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTPKVDKKVEPKSCDKTHTCPP- 234
Db 173 FPAVLQSD-LYTLSSSVTVTPSSVTPSETVTCNVAHPASSTKVVDKIVPRDCG----CKPC 227

QY 235 -CPAPELLGSPSVFLPFPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 293
Db 228 ICTVPEV--SSVFIFPPKPKDVLITITLTPKVTCTVVDISKDDPEVQFSWFVDDVEVHTA 284

QY 294 KTKPREEQYNSTYRVSVSLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQ 353
Db 285 QTQPREEQNSTFRSVSELPIMHQDWLNKGEYCKVSNAAFPAPIEKTISKGRPKAPQ 344

QY 354 VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGGSFFLY 413
Db 345 VYTIPTPPKEQMAKDKVSLTCTMITDFPEPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVY 404

QY 414 SKLTVDKSRWQGNVFSVCSVMHEALHNHYTQKSLSLSPGK 453
Db 405 SKLNVQKSNWEAGNTFTCSVLHSEGLHNHTEKSLSHSPGK 444

RESULT 7
S69339
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
A;Cross-references: EMBL:X81695
R;Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140,'C',142-374 <KH2>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 60.7%; Score 1477; DB 2; Length 374;
Best Local Similarity 63.5%; Pred. No. 7e-79;
Matches 289; Conservative 20; Mismatches 44; Indels 102; Gaps 3;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSIT--SGYSWNWIRQAPGKLEWVASITYDGSTN 59
Db 20 QITLKESGPTLVKPTQTTLTCTFSGFSLSKSGVGWIRQPPGQALEWLALIFWDDDKR 79

[illegible]

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RESULT 8
S22080
IG heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
N;Alternate names: IG gamma-1 chain C region (clone 8.10)
C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S22080; S06610; A31303

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A;Gene: Ig CH gamma-1
A;Introns: 98/1; 111/1; 221/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F;161-225/Domain: immunoglobulin homology <IMM>
F;318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          60.3%; Score 1467; DB 2; Length 470;
Best Local Similarity 62.6%; Pred. No. 3.5e-78;
Matches 286; Conservative 58; Mismatches 103; Indels 10; Gaps 8

Qy 1 EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSWNWIRQAPGKLEWVASITYDGSSTNY 60
    :||| ||| ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 20 QVQLRESGSPSLVKPSQTLSLTCTVSCFSLSS-YALTWVRQAPGKALEWVGITSGGTYY 78

Qy 61 ADSVKGRFTISRDDSKNTFY LQMNSLRAEDTAVYYCARGSH-YFGHWHPA-VWGQGTTLVT 118
    :|| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 79 NPALKSRLLSITKENS KSOVLSVSSVTPEDTATYYCARSTYGEVGDGALADAWQGGLLVT 138

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QY	119	VSSASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA	178
DB	139	VSSAST--TAPKVVPLSSCCGDKSSSTVTLGCLVSSYPPEPVTVWNSGALKSGVHTFPA	196
QY	179	VLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSNTKVDKKVEPKSKDKTHTCPPCPAP	238
DB	197	VLQSSGLYSLSSMVTVPGSTG-QTFTCNVAHPASSTKVDKAVDP-TC-KPSPCDCCPPP	253
QY	239	ELGGGPSVFLFPPKPDILMISRTPEVTCVAVDVSHEDPEVKFNWYVDGVEVHNAKTKPR	298
DB	254	ELPGGPSVFIFPPKPKDILTISGTPEVTCVAVDVGHDDPEVKFSWFVDDEVNTATTKPR	313
QY	299	EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP	358
DB	314	EEQFNSTYRVVVSALRIQHODWTGKGKEFKCKVHNEGLPAPIVTRTISRKGPAREPQVVLA	373
QY	359	PSREEMTKNQVSLTCLVKGYFSPVDIAVEWESNGQP--ENNYKTTTPVLDSGDSFFLYSKL	416
DB	374	PPQEELSKSTVSLTCLMWTSFYPDYIAVEWQRNGQPESEDKYGTTPQLDADSSYFLYSKL	433
QY	417	TVDKSRWQQGNVFPSCSVMHAEALHNHYTQKSLSLSPGK	453
DB	434	RVDNRNSWQEGDITYTCVVNVHEALHNHYTQKSTKSAGK	470

RESULT 9
S31459
Ig gamma-1 chain - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_charge 16-
C;Accession: S31459
R;Patrl, S.; Nau, F.
Submitted to the EMBL Data Library, December 1992
A;Reference number: S31459
A;Accession: S31459
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-472 <PAT>
A;Cross-references: EMBL:X69797
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;277-346/Domain: immunoglobulin homology <IMM>

Query Match	59.4%;	Score 1444;	DB 2;	Length 472;
Best Local Similarity	59.9%;	Pred. No. 7.5e-77;		
Matches 275; Conservative	64;	Mismatches 110;	Indels 10;	Gaps 5

QY	1	EVQLVESGGGLVQPGGSLRLS	CAVSGYSITSGYSWNWIR	QAPGKLEWVASITYDGS	TNY	60	
Db	18	QVRLQESG	PSLATLLQLT	SVTCTISG	FSL-NNYGVDWVRQAPGKALEWLGSGSYDEDIDY	76	
QY	61	ADSVKGRFTISRDDSKNTFYLQ	MNSLRAEDTAVYYCAR----	GSYFGHHHFAVWGQ	CTL	116	
Db	77	NPVLKSR	LSITKDTSKSQVSLTLSTVT	TEDTAVYYCARVDYDSSHAFA	YASYDFWGPGLL	136	
QY	117	VTVSSASTK	KGPSVFP	LAPSSKSTSGGTAALG	CLVKDYFPPEPVTVWNSGAL	TSGVHTF	176
Db	137	ISVLSAST--	TPPKVYPLTSCCGDTSSS	IVTLGCLVSSYMPEPVT	VTWNSGAL	TSGVHTF	194
QY	177	PAVLQSSGLYSLSVVTV	PSSSLGTQTYICNVNHKPSNTK	VDKVKVEPKSCDK	THTCPPCP	236	
Db	195	PAILQSSGLYSLSVVTV	PASTSGAQTFCINVAHPASSTK	VDKRVEPGCPD	PKCHC-RCP	253	
QY	237	APELLGGPSVFLFP	PKPXTLMISRTPEVTCVVDV	SHEDPEVKFNWYVDG	VEVHNAKTK	296	
Db	254	PPELPGGPSVFIFPP	KPKDTLTISGTPEVTCVVDV	GGDDPEVQSFVFNVEV	RTARTK	313	
QY	297	PREEQYNSTYRV	VSVLTVLH	QDWLNGKEYCKVSNKALP	APIEKTISKAKGQPREPQVY	356	
Db	314	PREEQFNSTFRV	VSALPIQH	QDWTGGKEFKCKVHNEALP	APIVTRISRTKGA	REPQVYV	373
QY	357	LPSSREEMTKNOVSLT	CLVKGYPSDIAVEWESNGOP--	ENNYKTTPTTVL	DSGSFFELYS	414	

Db 374 LAPPQELSKSTLSVTCLVTGFPDYIAVEWQKNGQPESEDKYGTTSQLDADGSYFLYS 433

Qy 415 KLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 453

Db 434 RLRVDKNSWQEGDTYACVMHEALHNHYTKQSLSPGK 472

RESULT 10

S37483

Ig gamma-2a chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S37483

R:Ducancel, F.F.D.

submitted to the EMBL Data Library, February 1993

A:Reference number: S37483

A:Accession: S37483

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-469 <DUC>

A:Cross-references: EMBL:X70423; NID:G406252; PIDN:CAA49868.1; PID:G406253

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin

F:276-345/Domain: immunoglobulin homology <IMM>

Query Match 57.7%; Score 1403.5; DB 2; Length 469;

Best Local Similarity 58.3%; Pred. No. 1.7e-74;

Matches 270; Conservative 68; Mismatches 102; Indels 23; Gaps 8;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWMWIRQAPGKLEWVASI-TYDGSNT 59

Db 20 QIQLOQSGPELVKPGASVKISCKASGYTFD-YVINWVKQPGQGLKWIGWIPASGNTK 78

Qy 60 YADSVKGRFTISRDDSKNTFYLQMNSLRAEDTAVYYCARGS-----HYFGHWHPAVWG 112

Db 79 YNENFKGKATLTVDTSSTAYMQLSSLTSEDYAVYFCARAMGATATLLDY-----WG 130

Qy 113 QGTLVTVSSASTKCGKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG 172

Db 131 QGTLTVTVSSAKT--TAPSVYPLAPVCGDITGSSVTGLGCLVKGYFPEPTVLTWNSGSLSSG 188

Qy 173 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNITKVDKKVEPKSCDKTHTC 232

Db 189 VHTFPAVLQSD-LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPC 246

Qy 233 PP--CPABELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 290

Db 247 PPKCKCPAPNLGGPSVFIAPPKIKDVLMSISLPIVTCVVVDVSEDDPDVQISFWFNNVEV 306

Qy 291 HNAKTKREEEQNSTYRVSVLTCLVHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPR 350

Db 307 HTAQTQTHREDYNSTLRVVSALPIQHQQDWSGKEFKCKVNNKDLPAPIERTISKPKGSVR 366

Qy 351 EPQVYTLPPSREEMTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLDSDGSF 410

Db 367 APQVYVLPPEEEMTKKQVTLTCMVTDMPEDIYVEWTNNGKTELNYKNTPEVLDSDGSY 426

Qy 411 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 453

Db 427 FMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSTRTPGK 469

RESULT 11

S40295

Ig gamma-2a chain (mab735) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999

C:Accession: S40295

R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bl

submitted to the EMBL Data Library, January 1993

A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against

A:Reference number: S40295

A:Accession: S40295

A:Molecule type: protein

A:Residues: 1-446 <KLE>

C:Genetics:

A:Map position: 12

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid

F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>

F:1-117/Domain: V-D-J region <VDJ>

F:118-446/Domain: C region <CHR>

F:118-214/Domain: C1 region <CH1>

F:215-230/Region: hinge

F:231-340/Domain: C2 region <CH2>

F:341-446/Domain: C3 region <CH3>

F:360-427/Domain: immunoglobulin homology <IMM>

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted

F:132/Disulfide bonds: interchain (to light chain) #status predicted

F:224,227,229/Disulfide bonds: interchain #status predicted

F:297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 57.7%; Score 1403; DB 2; Length 446;

Best Local Similarity 59.4%; Pred. No. 1.7e-74;

Matches 271; Conservative 67; Mismatches 104; Indels 14; Gaps 8;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWMWIRQAPGKLEWVASITYDGS--T 58

Db 1 QIQLOQSGPELVKPGASVKISCKASGYTFD-YVINWVKQPGEGLEWIGWI-YFSGNT 58

Qy 59 NYADSVKGRFTISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHPAVWGQGLVT 118

Db 59 KYNEKFKGKATLTVDTSSTAYMQLSSLTSEDYAVYFCARG---GKFAMDYWGQGTSTV 114

Qy 119 VSSASTKCGKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPA 178

Db 115 VSSAKT--TAPSVYPLAPVCGDITGSSVTGLGCLVKGYFPEPTVLTWNSGSLSSGVTFPA 172

Qy 179 VLQSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNITKVDKKVEPKSCDKTHTCPP--CP 236

Db 173 VLQSD-LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPPCKCP 230

Qy 237 APPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 296

Db 231 APNLLGGPSVFIAPPKIKDVLMSISLSPMVTCTVVVDVSEDDPDVQISFWFNNVEVLTAQTQ 290

Qy 297 PREEQYNSTYRVSVLTCLVHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYT 356

Db 291 THREDYNSTLRVVSALPIQHQQDWSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYV 350

Qy 357 LPPSREEMTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKL 416

Db 351 LPPPEEEMTKKQVTLTCMVTDMPEDIYVEWTNNGKTELNYKNTPEVLDSDGSYFMYSKL 410

Qy 417 TVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPG 452

Db 411 RVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSTRTPG 446

RESULT 12

G2MS11

Ig gamma-2b chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000

C:Accession: S25057; A02157; A26235; A26232; A26233; A53598

R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.

submitted to the EMBL Data Library, July 1992

A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific

A:Reference number: S25057

A:Accession: S25057

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-474 <FIS>

A:Cross-references: EMBL:X67210; NID:G54826; PIDN:CAA47649.1; PID:G54827

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:10:58 ; Search time 14.1773 Seconds
(without alignments)
1663.765 Million cell updates/sec

Title: US-09-925-179-8
Perfect score: 2432
Sequence: 1 EVQLVESGGGLVQPGGSLRL.....MHEALHNHYTQKSLSLSPGK 453

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1750	72.0	330	1	GC1_HUMAN	P01857 homo sapien
2	1599	65.7	326	1	GC2_HUMAN	P01859 homo sapien
3	1585.5	65.2	327	1	GC4_HUMAN	P01861 homo sapien
4	1231.5	50.6	323	1	GC_RABIT	P01870 oryctolagus
5	1202.5	49.4	329	1	GC2_CAVPO	P01862 cavia porce
6	1162	47.8	290	1	GC3_HUMAN	P01860 homo sapien
7	1150	47.3	326	1	GC1_RAT	P20759 rattus norv
8	1142	47.0	324	1	GC1_MOUSE	P01868 mus musculu
9	1142	47.0	329	1	GC3_MOUSE	P22436 mus musculu
10	1139.5	46.9	333	1	GCB_RAT	P20761 rattus norv
11	1137	46.8	393	1	GC1M_MOUSE	P01869 mus musculu
12	1131	46.5	398	1	GC3M_MOUSE	P03987 mus musculu
13	1126	46.3	330	1	GCA_MOUSE	P01863 mus musculu
14	1123.5	46.2	335	1	GCA_MOUSE	P01864 mus musculu
15	1121	46.1	399	1	GCAM_MOUSE	P01865 mus musculu
16	1117.5	45.9	329	1	GCC_RAT	P20762 rattus norv
17	1110	45.6	322	1	GCA_RAT	P20760 rattus norv
18	1082	44.5	336	1	GCB_MOUSE	P01866 mus musculu
19	1077	44.3	405	1	GCEM_MOUSE	P01867 mus musculu
20	482.5	19.8	429	1	EPC_RAT	P01855 rattus norv
21	478	19.7	428	1	EPC_HUMAN	P01854 homo sapien
22	468	19.2	421	1	EPC_MOUSE	P06336 mus musculu
23	441	18.1	454	1	MUC_HUMAN	P01871 homo sapien
24	439.5	18.1	122	1	HV3G_HUMAN	P01768 homo sapien
25	437.5	18.0	458	1	MUC_RABIT	P03988 oryctolagus
26	431.5	17.7	455	1	MUC_MOUSE	P01872 mus musculu
27	427.5	17.6	479	1	MUCM_RABIT	P04221 oryctolagus
28	421.5	17.3	476	1	MUCM_MOUSE	P01873 mus musculu
29	421	17.3	119	1	HV3I_HUMAN	P01770 homo sapien
30	420	17.3	123	1	HV24_MOUSE	P01793 mus musculu
31	419	17.2	120	1	HV3E_HUMAN	P01766 homo sapien
32	418	17.2	457	1	MUC_SUNMU	P20768 suncus muri
33	415.5	17.1	114	1	HV3B_HUMAN	P01763 homo sapien

ALIGNMENTS

RESULT 1

GC1_HUMAN						
ID	GC1_HUMAN	STANDARD;	PRT;	330 AA.		
AC	P01857;					
DT	21-JUL-1986 (Rel. 01, Created)					P01874 canis famil
DT	21-JUL-1986 (Rel. 01, Last sequence update)					P06337 mesocricetu
DT	15-MAR-2004 (Rel. 43, Last annotation update)					P01771 homo sapien
DE	Ig gamma-1 chain C region.					P01767 homo sapien
GN	IGHG1.					P01765 homo sapien
OS	Homo sapiens (Human).					P19181 carassius a
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					P01769 homo sapien
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					P01791 mus musculu
OX	NCBI_TaxID=9606;					P01781 homo sapien
RN	[1]					P01782 homo sapien
RP	SEQUENCE FROM N.A.					P01799 mus musculu
RX	MEDLINE=82274238; PubMed=6287432;					P04220 homo sapien
RA	Ellison J.W., Berson B.J., Hood L.E.;					
RT	"The nucleotide sequence of a human immunoglobulin C gamma gene."					
RL	Nucleic Acids Res. 10:4071-4079(1982).					
RN	[2]					
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).					
RX	MEDLINE=71064024; PubMed=5489771;					
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,					
RA	Waxdal M.J., Edelman G.M.;					
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino					
RT	acid sequence of heavy-chain cyanogen bromide fragments H1-H4."					
RL	Biochemistry 9:3161-3170(1970).					
RN	[3]					
RP	SEQUENCE OF 136-329 (EU).					
RX	MEDLINE=71064025; PubMed=5530842;					
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,					
RA	Edelman G.M.;					
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino					
RT	acid sequence of heavy-chain cyanogen bromide fragments H5-H7."					
RL	Biochemistry 9:3171-3181(1970).					
RN	[4]					
RP	SEQUENCE (MYELOMA PROTEIN NIE).					
RX	MEDLINE=77070269; PubMed=826475;					
RA	Ponstingl H., Hilschmann N.;					
RT	"The rule of antibody structure. The primary structure of a					
RT	monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The					
RT	chymotryptic peptides of the H-chain, alignment of the tryptic					
RT	peptides and discussion of the complete structure."					
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).					
RN	[5]					
RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.					
RX	MEDLINE=83289131; PubMed=6884994;					
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;					
RT	"Three-dimensional structure determination of antibodies. Primary					
RT	structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."					
RL	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).					
RN	[6]					
RP	DISULFIDE BONDS.					
RX	MEDLINE=71064027; PubMed=4923144;					
RA	Gall W.E., Edelman G.M.;					
RT	"The covalent structure of a human gamma G-immunoglobulin. X.					

RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
RN [7]
RP DISULFIDE BONDS.
RX MEDLINE=77070267; PubMed=1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
RT characterization of the protein, the L- and H-chains, the
RT cyanogen bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=81208100; PubMed=7236608;
RA Deisenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from Staphylococcus
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370(1981).
CC -!- MISCELLANEOUS: Nie has the GLM(17) allotypic marker, 97-K, and the
CC GLM(1) markers, 239-D and 241-L. KOL and EU sequences have the
CC GLM(3) marker and the GLM (non-1) markers.
CC -!- MISCELLANEOUS: Nie also differs in the amidation states of
CC 35, 116, 198, 269 and 272.
CC -!- MISCELLANEOUS: EU also differs in the amidation states of residues
CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues
CC 268-272.
CC -!- MISCELLANEOUS: KOL also differs in the amidation states of
CC residues 198, 267 and 272.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00228; AAC82527.1; ALT_INIT.
DR PIR; A93433; GHU.
DR PDB; 1FC1; 15-JUL-92.
DR PDB; 1FC2; 15-JUL-92.
DR PDB; 1AJ7; 12-NOV-97.
DR PDB; 1DSB; 09-FEB-00.
DR PDB; 1DSI; 09-FEB-00.
DR PDB; 1D6V; 04-OCT-00.
DR PDB; 1DN2; 17-MAY-00.
DR PDB; 1B4K; 06-JUN-01.
DR PDB; 1FCC; 20-JUL-95.
DR PDB; 1HZH; 12-JUN-02.
DR PDB; 1I72; 08-AUG-01.
DR PDB; 1IIS; 16-MAY-01.
DR PDB; 1IIX; 16-MAY-01.
DR PDB; 1L6X; 10-APR-02.
DR PDB; 2RCS; 12-NOV-97.
DR Genew; HGNC:5525; IGHG1.
DR MIM; 147100; -.
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; F:antigen binding; TAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW 3D-structure.
FT NON_TER 1 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 223 CH2.

FT DOMAIN 224 330
FT DISULFID 27 83
FT DISULFID 103 103
FT DISULFID 109 109
FT DISULFID 112 112
FT DISULFID 144 204
FT DISULFID 250 308
FT CARBOHYD 180 180
FT MOD RES 330 330
FT VARIANT 97 97
FT
FT VARIANT 239 239
FT
FT VARIANT 241 241
FT
FT STRAND 122 126
FT HELIX 130 134
FT TURN 136 137
FT STRAND 141 147
FT STRAND 157 162
FT TURN 163 164
FT STRAND 165 166
FT TURN 168 171
FT STRAND 176 179
FT TURN 180 181
FT STRAND 182 190
FT HELIX 193 197
FT TURN 198 199
FT STRAND 202 207
FT TURN 209 210
FT STRAND 215 219
FT STRAND 227 227
FT STRAND 230 234
FT HELIX 238 242
FT STRAND 245 256
FT STRAND 260 265
FT STRAND 270 270
FT STRAND 274 276
FT STRAND 280 281
FT TURN 283 284
FT STRAND 287 296
FT HELIX 297 301
FT TURN 302 303
FT STRAND 305 312
FT TURN 313 314
FT TURN 316 317
FT STRAND 320 325
SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;

Query Match 72.0%; Score 1750; DB 1; Length 330;
Best Local Similarity 98.8%; Pred.No. 4.7e-112;
Matches 328; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY 122 ASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQ 181
Db 1 AST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQ 58

QY 182 SSGLYSLSSVVTVFPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 241
Db 59 SSGLYSLSSVVTVFPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 118

QY 242 GGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 301
Db 119 GGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 178

QY 302 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 361
Db 179 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 238

QY 362 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 421
Db 239 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 298

CH3.
INTERCHAIN (WITH LIGHT CHAIN).
INTERCHAIN (WITH HEAVY CHAIN).
INTERCHAIN (WITH HEAVY CHAIN).

N-LINKED (GLCNAC...).
REMOVED POST-TRANSLATIONALLY.
K -> R (IN GLM(3) MARKER).
/FTid=VAR_003886.
D -> E (IN GLM(NON-1) MARKER).
/FTid=VAR_003887.
L -> M (IN GLM(NON-1) MARKER).
/FTid=VAR_003888.


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QY 422 RWQGNVFCSCVMHEALHNHYTKQSLSPGK 453
Db 299 RWQGNVFCSCVMHEALHNHYTKQSLSPGK 330

RESULT 2
GC2_HUMAN
ID GC2_HUMAN STANDARD; PRT; 326 AA.
AC P01859;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-2 chain C region.
GN IGHG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 2-326 FROM N.A.
RX MEDLINE=82197521; PubMed=6804948;
RA Ellison J.W., Hood L.E.;
RT "Linkage and sequence homology of two human immunoglobulin gamma
heavy chain constant region genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988 (1982).
RN [2]
RP SEQUENCE OF 88-115 FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=83001943; PubMed=6811139;
RA Takahashi N., Ueda S., Obata M., Nikaido T., Nakais., Honjo T.;
RT "Structure of human immunoglobulin gamma genes: implications for
evolution of a gene family.";
RL Cell 29:671-679 (1982).
RN [3]
RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=84235992; PubMed=6329676;
RA Krawinkel U., Rabbitts T.H.;
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
genes.";
RL EMBO J. 1:403-407 (1982).
RN [4]
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX MEDLINE=81007873; PubMed=6774012;
RA Wang A.-C., Tung E., Fudenberg H.H.;
RT "The primary structure of a human IGG2 heavy chain: genetic,
evolutionary, and functional implications.";
RL J. Immunol. 125:1048-1054 (1980).
RN [5]
RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX MEDLINE=80001357; PubMed=113060;
RA Connell G.E., Parr D.M., Hofmann T.;
RT "The amino acid sequences of the three heavy chain constant region
domains of a human IGG2 myeloma protein.";
RL Can. J. Biochem. 57:758-767 (1979).
RN [6]
RP SEQUENCE OF 238-275 (ZIE).
RX MEDLINE=80114419; PubMed=118920;
RA Hofmann T., Parr D.M.;
RT "A note of the amino acid sequence of residues 381-391 of human
immunoglobulins gamma chains.";
RL Mol. Immunol. 16:923-925 (1979).
RN [7]
RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
RA Hofmann T., Parr D.M.;
RL Submitted (MAR-1980) to the PIR data bank.
RN [8]
RP SEQUENCE OF 1-121 (DOT).
RX MEDLINE=95255298; PubMed=7737190;
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT "Characterization of the two unique human anti-flavon monoclonal
immunoglobulins.";

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FT  NON TER      1      1      INTERCHAIN (WITH A LIGHT CHAIN).
FT  DISULFID     16     16
FT  DISULFID     28     79
FT  DISULFID    105    105
FT  DISULFID    107    107
FT  DISULFID    110    110
FT  DISULFID    142    202
FT  CARBOHYD     178    178
FT  DISULFID    248    308
SQ  SEQUENCE   329 AA;  36074 MW;  5D231B7164D1FBA9 CRC64;

Query Match      49.4%;  Score 1202.5;  DB 1;  Length 329;
Best Local Similarity  69.2%;  Pred. No. 8e-75;
Matches 231;  Conservative 31;  Mismatches 63;  Indels 9;  Gaps 4;

QY  123 STKGKGPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 182
    | : ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  1 SARTTAPSVFPLAASCVDTSGMTLGLCLVKGYFPEPVTVKWSGALTSGVHTFPAVLQ- 59
    | : ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY  183 SGLYSLSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH--TCPPCPAPEL 240
    ||||| : ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db  60 SGLYSLSVTMTVPSSQKAT----CNVAHPASSTKVDKTVETIRTPZPBPTCPKCPPPEN 115
    ||||| : ||||| | | | | | | | | | | | | | | | | | | | | | | | |

QY  241 LGGPSVFLPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
    ||||| : ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db  116 LGGPSVFIFFPKPKDITLMISLTPTVTCVVVDVSDPEPEVQFTWFDNKPVGNAETKPRVE 175
    ||||| : ||||| | | | | | | | | | | | | | | | | | | | | | | | |

QY  301 QYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
    ||||| : ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db  176 QYNTTFRVESVLPVPIHQDWLRGKEFKCKVYNKALPAPIEKTISKTKGAPRMPDVYTLPPS 235

QY  361 REEMTKNQVSLTCLVKGYFSPVDIAVWESNGQP--ENNYKTTTPVLDSDGSFFLYSKLTV 418
    | : : : : : | : | : | : | | | | | | | | | | | | | | | | | | | |
Db  236 RDELSSKSVSVTCLINFPFADIHVEWASNRVPVSEKEYKNTPTPIEDADGSFFLYSKLTV 295
    | : : : : : | : | : | : | | | | | | | | | | | | | | | | | | | |

QY  419 DKSRWQGNVFCVSMHEALHNHYTQKSLSLSPG 452
    ||||| : ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db  296 DKSAWDQGTVTYTCVSMHEALHNHYTQKAISRSPG 329
    ||||| : ||||| | | | | | | | | | | | | | | | | | | | | | | | |
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RESULT 6
GC3_HUMAN
ID  GC3_HUMAN      STANDARD;          PRT;   290 AA.
AC  P01860;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  15-MAR-2004 (Rel. 43, Last annotation update)
DE  Ig gamma-3 chain C region (Heavy chain disease protein) (HDC).
GN IGHG3.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE (DISEASE PROTEIN WIS).
RX  MEDLINE=81021548; PubMed=6774747;
RA  Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
RT  "Primary structure of human gamma 3 immunoglobulin deletion mutant:
RL  gamma 3 heavy-chain disease protein Wis.";
RN  Biochemistry 19:4304-4308(1980).
RN  [2]
RP  REVISIONS TO 12-97 (PROTEIN WIS).
RX  MEDLINE=77118561; PubMed=402363;
RA  Michaelson T.E., Frangione B., Franklin E.C.;
RT  "Primary structure of the 'hinge' region of human IgG3. Probable
RT  quadruplication of a 15-amino acid residue basic unit.";
RN  J. Biol. Chem. 252:883-889(1977).
RN  [3]
RP  REVISIONS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN ZUC).
RX  MEDLINE=77021516; PubMed=823945;
RA  Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
RT  "The amino acid sequence of 'heavy chain disease' protein ZUC.
RT  Structure of the Fc fragment of immunoglobulin G3.";
```

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RL  Biochem. Biophys. Res. Commun. 71:907-914(1976).
RN  [4]
RP  SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
RX  MEDLINE=82247835; PubMed=6808505;
RA  Alexander A., Steinmetz M., Barritault D., Frangione B.,
RA  Franklin E.C., Hood L., Buxbaum J.N.;
RT  "Gamma Heavy chain disease in man: cDNA sequence supports partial
RT  gene deletion model.";
RL  Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
CC  -!- SUBUNIT: Dimer linked by 12 disulfide bonds; it has an extra
CC  interchain disulfide bond at position 7 in addition to the 11
CC  normally present in the hinge region.
CC  -!- MISCELLANEOUS: The heavy chain disease protein WIS is shown.
CC  -!- MISCELLANEOUS: The sequence of residues 42-76 was taken from the
CC  Ref.2.
CC  -!- MISCELLANEOUS: Disease protein WIS is lacking most of the V region
CC  and all of the CH1 region.
CC  -!- MISCELLANEOUS: Disease protein ZUC lack most of the V region, all
CC  of the CH1 region, and part of the hinge compared with normal
CC  gamma-3 heavy chains.
CC  -!- MISCELLANEOUS: Disease protein OMM may represent an allelic form
CC  or another gamma chain subclass.
CC  -!- MISCELLANEOUS: The hinge region in gamma-3 chains is about four
CC  times as long as in other gamma chains and contains three
CC  identical 15-residue segments preceded by a similar 17-residue
CC  segment (12-28).
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; J00231; AAA52805.1; ALT_SEQ.
DR  HSSP; P01857; 1FC1.
DR  Genew; HGNC:5527; IGHG3.
DR  MIM; 147120; -.
DR  GO; GO:0005624; C:membrane fraction; NAS.
DR  GO; GO:0003823; F:antigen binding; TAS.
DR  GO; GO:0006955; P:immune response; NAS.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003597; Ig_c1.
DR  InterPro; IPR003006; Ig_MHC.
DR  Pfam; PF00047; Ig; 2.
DR  SMART; SM00407; IGc1; 1.
DR  PROSITE; PS50835; IG_LIKE; 2.
DR  PROSITE; PS00290; IG_MHC; 1.
KW  Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat;
KW  Pyrrolidone carboxylic acid.
FT  DOMAIN      12    73      HINGE.
FT  DOMAIN      74    183     CH2.
FT  DOMAIN     184    289     CH3.
FT  REPEAT      29    43
FT  REPEAT      44    58
FT  REPEAT      59    73
FT  MOD_RES      1    1
FT  CARBOHYD      6    6
FT  DISULFID      7    7      INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT  DISULFID     24    24      INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT  DISULFID     27    27      INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT  DISULFID     33    33      INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT  DISULFID     39    39      INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT  DISULFID     42    42      INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT  DISULFID     48    48      INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT  DISULFID     54    54      INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT  DISULFID     57    57      INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT  DISULFID     63    63      INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT  DISULFID     69    69      INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT  DISULFID     72    72      INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT  CARBOHYD    140    140     N-LINKED (GLCNAC. . .).
FT  MOD_RES    290    290     REMOVED POST-TRANSLATIONALLY.
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FT VARIANT 126 127 QV -> EB (IN ZUC).
FT FTID=VAR 003890.
FT VARIANT 134 134 P -> L (IN OMM).
FT FTID=VAR 003891.
FT VARIANT 139 139 F -> Y (IN OMM).
FT FTID=VAR 003892.
FT VARIANT 182 182 T -> A (IN OMM).
FT FTID=VAR 003893.
FT VARIANT 227 227 S -> N (IN OMM).
FT FTID=VAR 003894.
FT VARIANT 227 227 MISSING (IN ZUC).
FT FTID=VAR 003895.
FT VARIANT 279 279 F -> Y (IN OMM).
FT FTID=VAR 003896.
SQ SEQUENCE 290 AA; 32331 MW; E69CBC95705B2F46 CRC64;

Query Match 47.8%; Score 1162; DB 1; Length 290;
Best Local Similarity 91.4%; Pred. No. 3.9e-72;
Matches 212; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 222 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKF 281
DB 59 EPKSCDTPPCRCPCAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVQF 118
QY 282 NWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 341
DB 119 KXYVDGVQHNAKTPREQQFNSTFRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 178
QY 342 ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 401
DB 179 ISKTGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTP 238
QY 402 PVLDSGGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453
DB 239 PMLDSGGSFFLYSKLTVDKSRWQGNIFSCSCVMHEALHNHRTQKSLSLSPGK 290
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RESULT 7
GC1_RAT
ID GC1_RAT STANDARD; PRT; 326 AA.
AC P20759;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0017; PS0017.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 112 HINGE.
FT DOMAIN 113 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
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FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 246 304
FT CARBOHYD 176 176 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

Query Match 47.3%; Score 1150; DB 1; Length 326;
Best Local Similarity 64.0%; Pred. No. 3e-71;
Matches 210; Conservative 51; Mismatches 57; Indels 10; Gaps 4;

QY 129 PSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYS 188
DB 6 PSVYPLAPGTALKSNSMVTGLCLVKGYFPEPTVTWNSGALSSGVHTFPAVLQ-SGLYTL 64
QY 189 SSVTVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPPELLGG--PS 245
DB 65 TSSVTVPSSTWPSQTTCNVNHPASSTKVDKKIVPRNCG--GDCKPC----ICTGSEVSS 118
QY 246 VFLEPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 305
DB 119 VFLEPPPKPKDVLITLTPKTCVVVDISQDDPEVHFSWFDVDEVHTAOTRPPPEQFNST 178
QY 306 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMT 365
DB 179 FRSVSELPILHQDWLNGRTFRCKVTSAAFSPSIEKTSKPEGRTOVPHVYTMSPTEEMT 238
QY 366 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSLKLTVDKSRWQ 425
DB 239 QNEVSIITCMVKGFYPPDIYVWQMNGQPQENYKNTPTMTDGTGSYFLYSLKLVKKEKMQ 298
QY 426 GNVFSCSVMEALHNHYTQKSLSLSPGK 453
DB 299 GNVFCSVLHEGLHNHTEKLSLSPGK 326
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RESULT 8
GC1_MOUSE
ID GC1_MOUSE STANDARD; PRT; 324 AA.
AC P01868;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ig gamma-1 chain C region secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX MEDLINE=80202559; PubMed=6769752;
RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
cloned in a bacterial plasmid.";
RL Gene 9:87-97(1980).
RN [3]
RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=80012837; PubMed=113776;
RA Rogers J., Clarke P., Salser W.;
RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
heavy chain.";
RL Nucleic Acids Res. 6:3305-3321(1979).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 21).
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RX MEDLINE=78242288; PubMed=98524;
RA Adetugbo K.;
RT "Evolution of immunoglobulin subclasses. Primary structure of a
RL murine myeloma gamma chain.";
RJ J. Biol. Chem. 253:6068-6075(1978).
RN [5]
RP DISULFIDE BONDS (MOPC 21).
RX MEDLINE=73008889; PubMed=5073237;
RA Svasti J.; Milstein C.;
RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";
RL Biochem. J. 126:837-850(1972).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Secreted;
CC IsoId=P01868-1; Sequence=Displayed;
CC Note=May be the major isoform;
CC Name=Membrane-bound;
CC IsoId=P01869-1; Sequence=External;
CC
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CC -----
DR EMBL; V00793; CAA24172.1; -;
DR EMBL; V00793; CAA24173.1; -;
DR EMBL; V00793; CAA24174.1; -;
DR EMBL; V00793; CAA24175.1; -;
DR EMBL; V00795; CAA24176.1; -;
DR PIR; A02159; GIMS.
DR GlycoSuiteDB; P01868; -;
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
FT FTId=CAR_000055.
FT
FT DISULFID 244 302
FT MOD_RES 324 324 REMOVED POST-TRANSLATIONALLY.
FT CONFLICT 276 276 N -> D (IN REF. 3).
FT CONFLICT 278 278 N -> D (IN REF. 3).
SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;
Query Match 47.0%; Score 1142; DB 1; Length 324;
Best Local Similarity 63.0%; Pred. No. 1e-70;
Matches 206; Conservative 54; Mismatches 57; Indels 10; Gaps 4;
QY 129 PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL 188
Db 6 PSVYPLAPGSAQAQNSMVTGLCLVKGYFPEPVTVTVNSGSLSSGVHTFPAVLQSD-LYTL 64
QY 189 SSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPP--CPAPELGGPSV 246

Db 65 SSSVTPSSPRPSETVTCNVAHPASSTKVKDKIVPRDCG-----CKPCICTVPEV---SSV 117
QY 247 FLPPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFKNWYVDGVEVHNAKTKPREEQYNSTY 306
Db 118 FIFPPKPKDVLITITLTPKVTCTVVDISKDDPEQFSWFEVDDVEVHTAQTQPREEQFNSTF 177
QY 307 RVYSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSREEMTK 366
Db 178 RVSSELPIMHQDWLNGKEYKCRVNSAAPPAPIEKTISKTKGRPKAPQVYTIPTPKPEQMAK 237
QY 367 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 426
Db 238 DKVSLTCTMITDFPPEITVEWQWNGQPAENYKNTQPMINTNGSYFYVSKLVQKSNWEAG 297
QY 427 NVFSCSVMHAEALHNHYTQKSLSLSPGK 453
Db 298 NTFCTSVLHEGLHNHHTKSLSHSPGK 324

RESULT 9

GC3_MOUSE
ID GC3_MOUSE STANDARD; PRT; 329 AA.
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region, secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A.; Word C.J.; Rimm D.; Der-Balan G.P.; Martinez H.M.;
RA Tucker P.W.; Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00451; -; NOT_ANNOTATED_CDS.
DR PIR; B02156; G3MSC.
DR HSSP; P01857; IFC1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 47.0%; Score 1142; DB 1; Length 329;
Best Local Similarity 65.1%; Pred. No. 1e-70;
Matches 213; Conservative 44; Mismatches 66; Indels 4; Gaps 3;
QY 129 PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL 188

Db	5	PSVYPLVPGCSDTSGSSVTLGCLVKGYFPEPVTVKWNYGALSSGVRTVSSVLQ-SGFYSL	63
Qy	189	SSVTVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCP--PCPAPELLGGPSV	246
Db	64	SSLVTVPSSTWPSQTVICNVNHHKPSNTKVDKKVERNGGIGHKCPCTCTCHKCPVPELLG	122
Qy	247	FLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY	306
Db	123	FIFPPKPKDALMISLTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTF	182
Qy	307	RVVSVLTVTLVHODWLNKGKVKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK	366
Db	183	RVVSALPIQHODWMRGKEFKCKVVKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK	242
Qy	367	NQVSLTCLVKGFYPSPDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG	426
Db	243	KKVSLTCLVNTFFSEAIISWEVERNGELEDYKNTTPPILDSGDGTFLYSLKLTVDTSWLQ	302
Qy	427	NVPSCSVMHEALHNHYTQKSLSLSPGK	453
Db	303	EFTCSVVHEALHNHHTQKLSRSPGK	329
RESULT 10			
GCB_RAT			
ID	GCB_RAT	STANDARD;	PRT; 333 AA.
AC	P20761;		
DT	01-FEB-1991 (Rel. 17, Created)		
DT	01-FEB-1991 (Rel. 17, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Ig gamma-2B chain C region.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=89232738; PubMed=3149946;		
RA	Brueggemann M.;		
RT	"Evolution of the rat immunoglobulin gamma heavy-chain gene family.";		
RL	Gene 74:473-482(1988).		
CC	-!- SIMILARITY: Contains 3 immunoglobulin-like domains.		
DR	PIR; PS0018; PS0018.		
DR	HSSP; P01842; 7FAB.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003597; Ig cl.		
DR	InterPro; IPR003006; Ig_MHC.		
DR	Pfam; PF00047; Ig; 3.		
DR	SMART; SM00407; Igcl; 2.		
DR	PROSITE; PS50835; IG_LIKE; 3.		
DR	PROSITE; PS00290; IG_MHC; 1.		
KW	Immunoglobulin domain; Immunoglobulin C region; Repeat.		
FT	NON_TER 1		
FT	DOMAIN 6 96		IG-LIKE 1.
FT	DOMAIN 124 223		IG-LIKE 2.
FT	DOMAIN 232 328		IG-LIKE 3.
FT	DISULFID 15 15		INTERCHAIN (WITH A LIGHT CHAIN).
FT	DISULFID 27 80		
FT	DISULFID 106 106		INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 109 109		INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 112 112		INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 115 115		INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 147 207		
FT	DISULFID 253 311		
SQ	SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;		
Query Match 46.9%; Score 1139.5; DB 1; Length 333;			
Best Local Similarity 64.4%; Pred. No. 1.6e-70;			
Matches 213; Conservative 44; Mismatches 65; Indels 9; Gaps 3;			
Qy	129	PSVFPPLAPSSKSTSGTAALGCLVKDYFPPVTVSWNSGALTSGVHTFPAVLQSSGLYSL	188
Db	6	PSVYPLAPGCGDTTSSSTVTLGCLVKGYFPEPVTVWNSGALSSDVHTFPAVLQ-SGLYTL	64

Qy	189	SSVTVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKS-----CDKTHTCPPCPAPPELLG	242
Db	65	TSSVT--SSTWPSQTVTCNVNHHKPSNTKVDKKVERNGGIGHKCPCTCTCHKCPVPELLG	122
Qy	243	GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY	302
Db	123	GPSVFIFFPKPKDILLISQNAKVTVCVVVDVSEEDPDVQFSWFWNNVEVHTAQTPREEQY	182
Qy	303	NSTVRVSVLTVTLVHODWLNKGKVKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE	362
Db	183	NSTFRVVSALPIQHODWMSGKEFKCKVVKVSNKALPAPIEKTISKPKGLVRKPVVYMGPPTE	242
Qy	363	EMTKNQVSLTCLVKGFYPSPDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR	422
Db	243	QLTEQIVSLTCLTSGFLPNDIGVEWTSNGHIEKNYKNTPEVMDSDGSFFMYSKLNVRSR	302
Qy	423	WQGNVPSCSVMHEALHNHYTQKSLSLSPGK	453
Db	303	WDSRAPFVCSVVHEGLHNHVEKSISSRPPGK	333
RESULT 11			
GCM_MOUSE			
ID	GCM_MOUSE	STANDARD;	PRT; 393 AA.
AC	P01869;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	01-AUG-1991 (Rel. 19, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Ig gamma-1 chain C region, membrane-bound form.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=80045036; PubMed=115593;		
RA	Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,		
RA	Takahashi N., Mano Y.;		
RT	"Cloning and complete nucleotide sequence of mouse immunoglobulin		
RT	gamma 1 chain gene.";		
RL	Cell 18:559-568(1979).		
RN	[2]		
RP	SEQUENCE OF 323-393 FROM N.A.		
RX	MEDLINE=82197626; PubMed=6804950;		
RA	Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;		
RT	"mRNA for surface immunoglobulin gamma chains encodes a highly		
RT	conserved transmembrane sequence and a 28-residue intracellular		
RT	domain.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).		
RN	[3]		
RP	SEQUENCE OF 323-366 FROM N.A.		
RX	MEDLINE=82115295; PubMed=6799207;		
RA	Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,		
RA	Eisenberg D., Wall R.;		
RT	"Gene segments encoding transmembrane carboxyl termini of		
RT	immunoglobulin gamma chains.";		
RL	Cell 26:19-27(1981).		
RN	[4]		
RP	SEQUENCE OF 1-44 FROM N.A.		
RX	MEDLINE=82222190; PubMed=6283537;		
RA	Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;		
RT	"Nucleotide sequences of gene segments encoding membrane domains of		
RT	immunoglobulin gamma chains.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).		
CC	-!- ALTERNATIVE PRODUCTS:		
CC	Event=Alternative splicing; Named isoforms=2;		
CC	Name=Membrane-bound;		
CC	Isoid=P01869-1; Sequence=Displayed;		
CC	Name=Secreted;		
CC	Isoid=P01868-1; Sequence=External;		
CC	Note=May be the major isoform;		

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Db 64 SSVLVPSSTWPSQTVICNVAHASKTELKRIEPR-IPKSTPPGSSCPPGNILGPSV 122
QY 247 FLRPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 306
Db 123 FIFPPKPKDALMISLTQKVTCTCVVDVSEDDPDVHVSFVFNKEVHTAWTQPREAQYNSTF 182
QY 307 RVVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK 366
Db 183 RVVSALPIQHODWMRGKEFKCKVNNKALPAPIERTISKPKGRAQTPQVYTIPTPREQMSK 242
QY 367 NOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQG 426
Db 243 KKVSILTCLVNTFFSESAISVEWERNGELEQDYKNTTPILDSDGTFTFLYSKLTVDTSWLG 302
QY 427 NVFSCSVNHEALHNHYTQKSLSLSP 451
Db 303 EIFTCSVVHEALHNHHTQKNLSRSP 327

RESULT 13
GCAA_MOUSE STANDARD; PRT; 330 AA.
ID GCAA_MOUSE
AC P01863;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig gamma-2A chain C region, A allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81076554; PubMed=6777755;
RA Sikorav J.-L., Auffray C., Rougeon F.;
RT "Structure of the constant and 3' untranslated regions of the murine
RT Balb/c gamma 2a heavy chain messenger RNA.";
RL Nucleic Acids Res. 8:3143-3155(1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=81198976; PubMed=6262729;
RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;
RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
RT and evolution of heavy chain genes: further evidence for intervening
RT sequence-mediated domain transfer.";
RL Nucleic Acids Res. 9:1365-1381(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=81223894; PubMed=6787604;
RA Ollo R., Auffray C., Mochamps C., Rougeon F.;
RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
RT suggests that exons can be exchanged between genes in a multigenic
RT family.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
RN [4]
RP MYELOMA PROTEIN MOPC 173.
RX MEDLINE=74175517; PubMed=4831970;
RA Bourgois A., Fougereau M., Rocca-Serra J.;
RT "Determination of the primary structure of a mouse IgG2a
RT immunoglobulin: amino-acid sequence of the Fc fragment. Implications
RT for the evolution of immunoglobulin structure and function.";
RL Eur. J. Biochem. 43:423-435(1974).
RN [5]
RP DISULFIDE BONDS.
RX MEDLINE=73056887; PubMed=4565406;
RA de Preval C., Fougereau M.;
RT "Determination of the primary structure of a mouse gamma G2a
RT immunoglobulin. Identification of the disulfide bridges.";
RL Eur. J. Biochem. 30:452-462(1972).
CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC -----
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CC -----
DR EMBL; V00798; CAA24178.1; -.
DR PIR; A02152; G2MSA.
DR PDB; 1E4W; 12-JUL-01.
DR PDB; 1E4X; 12-JUL-01.
DR PDB; 1MNU; 06-MAY-99.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00407; Igcl; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure; Repeat.
FT NON TER 1
FT DOMAIN 6 98 IG-LIKE 1.
FT DOMAIN 121 220 IG-LIKE 2.
FT DOMAIN 229 325 IG-LIKE 3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT MOD RES 330 330 REMOVED POST-TRANSLATIONALLY.
SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;

Query Match 46.3%; Score 1126; DB 1; Length 330;
Best Local Similarity 64.0%; Pred. No. 1.3e-69;
Matches 212; Conservative 42; Mismatches 73; Indels 4; Gaps 3;

QY 125 KGKGPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 184
Db 2 KTTAPSVYPLAPVCGDTTSSSVTLGCLVKGYFPEPTVLTWNSGSLSSGVHTFPAVLQSD- 60
QY 185 LYSLSVVTVPSSSLGTTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP--CPAPELIG 242
Db 61 LYTLLSSVTVTSSTWPSQSIITCNVAHPASSTKVDKKEPRG-PTIKPCPPCKCPAPNLLG 119
QY 243 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 302
Db 120 GPSVFIFFPKIKDVLMSLSPITCVVDVSEDDPDVQISWFVNVEVHTAQQTTHREDY 179
QY 303 NSTYRVVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE 362
Db 180 NSTLRVVSALPIQHODWMSGKEFKCKVNNKDLPAPIERTISKPGSVRAPQVYVLPPEE 239
QY 363 EMTKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSR 422
Db 240 EMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTPEPVLDSGYSFYMSKLRVEKKN 299
QY 423 WQGNVFPSCSVNHEALHNHYTQKSLSLSPGK 453
Db 300 WVERNYSVCSVVHEGLHNHHTTKSFRTPGK 330

RESULT 14
GCAAB_MOUSE STANDARD; PRT; 335 AA.
ID GCAAB_MOUSE
AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ig gamma-2A chain C region secreted form (B allele).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:36:43 ; Search time 48.608 Seconds
(without alignments)
2940.454 Million cell updates/sec

Title: US-09-925-179-8
Perfect score: 2432
Sequence: 1 EVQLVESGGGLVQPGGSLRL.....MHEALHNHYTQKSLSLSPGK 453

Scoring table: BLOSUM62
Gapop 10.0., Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2153	88.5	470	4 Q7Z5W1	Q7z5w1 homo sapien
2	2115	87.0	482	4 Q7Z351	Q7z351 homo sapien
3	2043.5	84.0	469	4 Q7Z7P5	Q7z7p5 homo sapien
4	2019.5	83.0	521	4 Q8N4Y9	Q8n4y9 homo sapien
5	1903	78.2	473	4 Q8TC63	Q8tc63 homo sapien
6	1611.5	66.3	509	4 Q8NF17	Q8nf17 homo sapien
7	1552.5	63.8	469	11 Q8R3V9	Q8r3v9 mus musculu
8	1530.5	62.9	354	4 Q86TT2	Q86tt2 homo sapien
9	1511.5	62.2	437	11 Q9RIA4	Q9rla4 mus musculu
10	1469.5	60.4	463	11 Q99LC4	Q99lc4 mus musculu
11	1463.5	60.2	473	11 Q91Z05	Q91z05 mus musculu
12	1458	60.0	470	11 Q7TMK1	Q7tmk1 mus musculu
13	1450.5	59.6	473	11 Q9D8L4	Q9d8l4 mus musculu
14	1424	58.6	468	11 Q99L31	Q99l31 mus musculu
15	1423.5	58.5	473	11 Q99L25	Q99l25 mus musculu
16	1371	56.4	474	11 Q8R3H6	Q8r3h6 mus musculu

17	1258	51.7	679	4 Q96PQ8	Q96pq8 homo sapien
18	1249.5	51.4	337	6 Q95M34	Q95m34 equus cabal
19	875.5	36.0	597	4 Q96BB9	Q96bb9 homo sapien
20	872	35.9	613	4 Q8WUK1	Q8wuk1 homo sapien
21	799.5	32.9	499	4 Q8N5K4	Q8n5k4 homo sapien
22	795	32.7	494	4 Q96K68	Q96k68 homo sapien
23	793.5	32.6	493	4 Q8NCL6	Q8nc16 homo sapien
24	765.5	31.5	487	11 Q99KA4	Q99ka4 mus musculu
25	762	31.3	486	11 Q91Z07	Q91z07 mus musculu
26	759.5	31.2	597	4 Q9BU10	Q9bu10 homo sapien
27	757.5	31.1	614	4 Q96GA6	Q96ga6 homo sapien
28	755.5	31.1	487	11 Q80Z17	Q80zi7 mus musculu
29	753.5	31.0	597	4 Q9BQB8	Q9bqb8 homo sapien
30	750	30.8	613	4 Q96EY0	Q96ey0 homo sapien
31	749.5	30.8	588	4 Q8WUX4	Q8wux4 homo sapien
32	749.5	30.8	618	4 Q96AA6	Q96aa6 homo sapien
33	738.5	30.4	614	11 Q7TMT6	Q7tmt6 mus musculu
34	735.5	30.2	480	11 Q91XE1	Q91xe1 mus musculu
35	731.5	30.1	479	11 Q91WP5	Q91wp5 mus musculu
36	729	30.0	613	11 Q8VCX7	Q8vcx7 mus musculu
37	726	29.9	278	11 Q921K1	Q921k1 mus musculu
38	726	29.9	479	11 Q99M22	Q99m22 mus musculu
39	719.5	29.6	478	4 Q7Z379	Q7z379 homo sapien
40	705	29.0	484	11 Q8VEA0	Q8vea0 mus musculu
41	700	28.8	492	4 Q7Z374	Q7z374 homo sapien
42	688	28.3	496	4 Q96KX8	Q96kx8 homo sapien
43	679	27.9	496	4 Q96DK0	Q96dk0 homo sapien
44	678.5	27.9	479	11 Q7TMK4	Q7tmk4 mus musculu
45	674	27.7	482	11 Q91X92	Q91x92 mus musculu

ALIGNMENTS

RESULT 1
Q7Z5W1
ID Q7Z5W1 PRELIMINARY; PRT; 470 AA.
AC Q7Z5W1;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=2238257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;

SQ	SEQUENCE	469 AA;	51395 MW;	C8D5BE12BAAF795C CRC64;
	Query Match	84.0%;	Score 2043.5;	DB 4; Length 469;
	Best Local Similarity	85.5%;	Pred. No. 4.7e-160;	
	Matches 389;	Conservative 25;	Mismatches 34;	Indels 7; Gaps 5;
QY	1	EVQLVESGGGLVQPGGSLRLS	CAVSGYSITSGYSWNWIRQAPGKGLEWVASIT-VDGSTN	59
Dd	20	QVHLVQSGAEVKKGASVKLSCKTSGYNFSS-YDLIWRQAPQGQLEWMGWISAHNGDTK	78	
QY	60	YADSVKGRFTISRDDSKNTFYIQMNSLRAEDTAVYYCARGSHYFGH-WHFVWGQGTLVLT	118	
Dd	79	YARKFQGRVTMTTDSATTSYMEFRSLRSDDTALFYCATKSR--GVGDFFDSWGQGTLLVT	136	
QY	119	VSSASTKGKGPSVFPLPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA	178	
Dd	137	VSSAST--KGPSVFPLPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA	194	
QY	179	VLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP	238	
Dd	195	VLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP	254	
QY	239	ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDDEVKFENWYVDGEVHNAKTKPR	298	
Dd	255	ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDDEVKFENWYVDGEVHNAKTKPR	314	
QY	299	EEQYNSTYRVVSVLTVLHQDWLNGKEYCKKVSNKALPAPIEKTISKAKGQPREPQVYTLIP	358	
Dd	315	EEQYNSTYRVVSVLTVLHQDWLNGKEYCKKVSNKALPAPIEKTISKAKGQPREPQVYTLIP	374	
QY	359	PSREEMTKNQVSLTCLVKGFYPSPDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV	418	
Dd	375	PSRDELTKNQVSLTCLVKGFYPSPDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV	434	
QY	419	DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	453	
Dd	435	DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	469	

RESULT	4
Q8N4Y9	PRELIMINARY; PRT; 521 AA.
ID	Q8N4Y9
AC	Q8N4Y9;
DT	01-OCT-2002 (TrEMBLrel. 22, Created)
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Hypothetical protein.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute-
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Primary B-Cells;
RA	Strausberg R.;
RL	Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; BC033178; AAH33178.1; -.
DR	PIR; A60764; A60764.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003597; Ig cl.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF00047; ig; 4.
DR	SMART; SMC0407; IGcl; 3.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PS50835; IG LIKE; 4.
DR	PROSITE; PS00290; IG_MHC; 2.
KW	Hypothetical protein.
SQ	SEQUENCE 521 AA; 57156 MW; 2AC7D2D2E72D6CAA2 CRC64;

QY	1	EVQLVESGGGLVQPGGSLRLSCA	VGYSITSGYSNNWIRQAPGKGLEWVA	---	SITYDGS	57
		:	:		:	
Db	20	EVQLVDSGGGLVQPGGSLRLSCA	ASGFIVSDHYV-EWVRQAPGKGP	EWVVCFRSKAHKST	78	
		:	:		:	
QY	58	TNYADSVKGRFTISRDDSKNTFY	LQMNLSRAEDTAVYICARGSHYFG	-	HWHPAVWGQGT	115
		:	:		:	
Db	79	TEYAAASVKGRFTLRDDSKNSVH	LQMNLSLKTDDTAVYICVRDLEGAGKYD	WYFDIWRGRI	138	
		:	:		:	
QY	116	LVTVSSASTKGGPSVFPEPLAPSS	KSTSGGTAALGCLVKDYFPEP	PTVTSWNSGALTSGVHT	175	
		:	:		:	
Db	139	LVTVSSAST--KGPSVFPEPLAPCSR	STSGGTAALGCLVKDYFPEP	PTVTSWNSGALTSGVHT	196	
		:	:		:	
QY	176	FPAVLQSSGLYSLSVVTVPS	SSSLGTQTYICNVNHKPSNTKVDKKV	-----	221	
		:	:		:	
Db	197	FPAVLQSSGLYSLSVVTVPS	SSSLGTQTYTCNVNHKPSNTKVDK	RVELKTPGLDTHTCP	256	
		:	:		:	
QY	222	-----	-----	-----	-----	
		:	:		:	
Db	257	RCPEPKSCDTPPPCPRCEPKSCD	TPPPCPRCEPKSCDTPPPCPRCP	APPELLGGPSVFL	316	
		:	:		:	
QY	249	FPPKPKDTLMISRTPEVTCVVVDV	SHEDPEVKFNWYVDGVEVHNAKTK	PREEQYNSTYRV	308	
		:	:		:	
Db	317	FPPKPKDTLMISRTPEVTCVVVDV	SHEDPEVQFKWYVDGVEVHNAKTK	PREEQFNSTFRV	376	
		:	:		:	
QY	309	VSVLTVLHQDWLNGKEYCKVSNKAL	PAPIEKTISKAKGQPREPPQVYTL	PPSREEMTKNQ	368	
		:	:		:	
Db	377	VSVLTVLHQDWLNGKEYCKVSNKAL	PAPIEKTISKAKGQPREPPQVYTL	PPSREEMTKNQ	436	
		:	:		:	
QY	369	VSLTCLVKGFYPSDIAVEWESNGQ	PENNYKTTTPPVLDSDGSFFLYSKLT	IVDKSRWQOQNV	428	
		:	:		:	
Db	437	VSLTCLVKGFYPSDIAVEWESNGQ	PENNYNTTTPPMLDSDGSFFLYSKLT	IVDKSRWQOQNI	496	
		:	:		:	
QY	429	FSCSVMEALHNHYTQKSLSLSPGK	453			
		:	:		:	
Db	497	FSCSVMEALHNRYTQKSLSLSPGK	521			
		:	:		:	

```

RESULT 5
Q8TC63
Q8TC63 PRELIMINARY; PRT; 473 AA.
AC Q8TC63;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AAH25985.1; -.
DR GO; GO:0005507; F:copper ion binding; IEA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000923; BlueCu 1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003396; Ig_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00196; COPPER BLUE; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;
Query Match 78.2%; Score 1903; DB 4; Length 473;
Best Local Similarity 80.4%; Pred. No. 1.9e-148;

```


Db 227 V---SSVFI PPPKPKDVLTTITLTPKVT CVVVVDISKDDPEVQFSWFVDDVEVHTAQTPRE 283

Qy 300 EQNSTYRVVSVLTVLHQDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPP 359

Db 284 EQNSTFRSVSELPIMHQDLNGKEFKCRVNSAAPAPIEKTISKTKGRKAPQVYITIPP 343

Qy 360 SRBEMTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 419

Db 344 PKQMAKDKVSLTCMITDFPFEDITVEQWNGQPAENYKNTQPIMDTDGSYFYSKLVNQ 403

Qy 420 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453

Db 404 KSNWEAGNTFTCSVLHEGLHNHHTEKNLSHSPGK 437

RESULT 10

Q99LC4

ID Q99LC4 PRELIMINARY; PRT; 463 AA.

AC Q99LC4;

DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Similar to RIKEN cdna 1810060009 gene.

GN IGH-4.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC003435; AAH03435.1; -.

DR PIR; B45837; B45837.

DR HSSP; P01842; 7FAB.

DR MGD; MGI:96446; Igh-4.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; ig; 3.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG LIKE; 4.

DR PROSITE; PS00290; IG_MHC; 1.

SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BEC30783 CRC64;

Query Match 60.4%; Score 1469.5; DB 11; Length 463;

Best Local Similarity 60.0%; Pred. No. 1.1e-112;

Matches 274; Conservative 77; Mismatches 89; Indels 17; Gaps 9;

Qy 1 EVLVESGGGLVQPGGSLRLSCAIVGYSITSGYSNWIRQAPGKLEWVASITVDGSTN- 59

Db 20 QVQLQSGAELARPGASVRLSCKASCTFT-GYGVSWVKQRTQGLEWVGEI-YPGSGNT 77

Qy 60 -YADSVKGRFTISRDDSKNTFYLQWNSLRAEDTAVYYCARGSHYFGHWFAVWGQTLVT 118

Db 78 YYSEKFKGKATLTIDKSSSTAYMHLSSLTSEDSAVYFCARSS-YYSYDLFAYWGQTLVT 136

Qy 119 VSSASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSVHTFPA 178

Db 137 VSAAKT--TPPSVYPLAPGSAAQTNMVTLGCLVKGYFPEPVTVSNWNSGSLSSGVHTFPA 194

Qy 179 VLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTPP--CP 236

Db 195 VLQSD-LYTLSSSVTVPPSSSTWPSSTWPSSTWPSSTWPSSTWPSSTWPSSTWPSSTWPS 249

Qy 237 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK 296

Db 250 VPEV---SSVFI PPPKPKDVLTTITLTPKVT CVVVVDISKDDPEVQFSWFVDDVEVHTAQ 306

Qy 297 PREEQYNSIRVSVSLTVLHQDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 356

Db 307 PREEQFNSTFRSVSELPIMHQDLNGKEFKCRVNSAAPAPIEKTISKTKGRKAPQVYT 366

Qy 357 LPPSREEMTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 416

Db 367 IPPPKEQMAKDKVSLTCMITDFPFEDITVEQWNGQPAENYKNTQPIMDTDGSYFYSKL 426

Qy 417 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453

Db 427 NVQKSNWEAGNTFTCSVLHEGLHNHHTEKLSHSPGK 463

RESULT 11

Q91Z05

ID Q91Z05 PRELIMINARY; PRT; 473 AA.

AC Q91Z05;

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Hypothetical protein.

GN AU044919.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC010327; AAH10327.1; -.

DR MGD; MGI:2144967; AU044919.

DR GO; GO:0005489; F:electron transporter activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR000345; CytC heme_BS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; ig; 3.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00190; CYTOCHROME C; 1.

DR PROSITE; PS50835; IG LIKE; 4.

DR PROSITE; PS00290; IG_MHC; 1.

KW Hypothetical protein.

SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 60.2%; Score 1463.5; DB 11; Length 473;

Best Local Similarity 61.6%; Pred. No. 3.4e-112;

Matches 286; Conservative 62; Mismatches 95; Indels 21; Gaps 9;

Qy 1 EVLVESGGGLVQPGGSLRLSCAIVGYSITSGYSNWIRQAPGKLEWVASITVDGSTN- 59

Db 20 EVLVESGGGLVQPGGSRKLSCAASGFTF-SDYGMHWVRQAPKLEWVAYIN-SGSTTI 77

Qy 60 -YADSVKGRFTISRDDSKNTFYLQWNSLRAEDTAVYYCARGSHYFGHW--HFAVWGQTL 116

Db 78 YYADTVKGRFTISRDNAXNTLFLQMTSLRSEDATMIYCAREL----WLRRIDYWGQTT 132

Qy 117 VTVSASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSVHTF 176

Db 133 ITVSSAKT--TPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPEPVTVSNWNSGSLSSVHTF 190

Qy 177 PAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT-HTCIPP- 234

Db 191 PALLQ-SGLYTMSSSVTVPPSSSTWPSQTVCVAHPASSTTVDDKKLEPSGPISTINPCPPC 249

Qy 235 -----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVE 289

Db 250 KECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVT CVVVVDVSEDDPDVQISWFWNVVE 309

Qy 290 VHNATKPREEQYNSTYRVSVSLTVLHQDLNGKEYKCKVSNKALPAPIEKTISKAKGQP 349

Db 310 VHTAQIQTREDYNSTIRVVSALPIQHQDWMNSGKEPKCKVNNKDLPSPIERTISKIKGLV 369

Qy 350 REPOVYTLPPSREEMTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTPPVLDSDGS 409

Db 370 RAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVENTSNHGTEENYKDTAPVLDSDGS 429

Db315TQTHREDYNSTLRVVSALPIQHODWMSGKEFKCKVNNKALPAPIERTISKPGSVRAPQV374

Qy355YTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS414

Db375YVLPPEEEMTKKQVTLTCMTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYS434

Qy415KLTVDKSRWQOQNVFSCSVMEALHNHYTQKSLSLSPGK453

Db435KLRVEKNWVERNSYSCSVTHEGLHNHHTTKSFSTRPCK473

Search completed: May 13, 2004, 15:47:21

Job time : 50.608 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:08:53 ; Search time 32.8137 Seconds
(without alignments)
1877.123 Million cell updates/sec

Title: US-09-925-179-9
Perfect score: 1135
Sequence: 1 DIQLTQSPSSLSASVGRVT.....EVTHQGLSSPVTXSNRGEK 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	1135	100.0	218	2	AAW95658	Mus muscu
2	1135	100.0	218	3	AAY85200	Aay85200 Light cha
3	1135	100.0	218	4	AAB76947	Aab76947 Full vari
4	1128	99.4	218	2	AAR33312	Aar33312 Humanised
5	1112	98.0	218	2	AAW95660	AAW95660 Mus muscu
6	1112	98.0	218	2	AAW95662	AAW95662 Mus muscu
7	1112	98.0	218	2	AAY50030	Aay50030 Human E27
8	1112	98.0	218	3	AAB07472	Aab07472 Amino aci
9	1112	98.0	218	4	AAB74211	Aab74211 E27 anti-
10	1112	98.0	218	6	ABU62797	Abu62797 E27 anti-
11	1109	97.7	218	2	AAW95664	AAW95664 Mus muscu
12	1109	97.7	218	2	AAW95669	AAW95669 Mus muscu
13	1109	97.7	218	4	AAB47087	Aab47087 Anti-IgE
14	1109	97.7	218	4	AAB76949	Aab76949 Full leng
15	1109	97.7	218	4	AAB76951	Aab76951 Full leng
16	1109	97.7	218	4	AAB76953	Aab76953 Variable
17	1109	97.7	218	4	AAB76958	Aab76958 Variable
18	1108	97.6	218	2	AAW13563	AAW13563 Humanised
19	1100	96.9	238	3	AAW90930	AAW90930 Humanised
20	1100	96.9	238	5	ABB74899	Abb74899 Humanised
21	1099	96.8	238	3	AAW90932	AAW90932 Humanised
22	1099	96.8	238	5	ABB74901	Abb74901 Humanised
23	1096	96.6	238	3	AAW90931	AAW90931 Humanised
24	1096	96.6	238	5	ABB74900	Abb74900 Humanised
25	1036	91.3	214	3	AAY93735	The Kappa

26	1036	91.3	214	6	AAE35890	Human 11.
27	1036	91.3	238	2	AAW83034	Anti-Fas
28	1036	91.3	238	3	AAB14777	Humanised
29	1036	91.3	238	3	AAW90927	Humanised
30	1036	91.3	238	5	ABB74942	Humanised
31	1036	91.3	238	5	ABB74896	Humanised
32	1031.5	90.9	237	3	AAY96298	Human IGF
33	1031	90.8	238	2	AAW83031	Anti-Fas
34	1031	90.8	238	3	AAB14772	Humanised
35	1031	90.8	238	3	AAW90922	Humanised
36	1031	90.8	238	5	ABB74937	Humanised
37	1031	90.8	238	5	ABB74891	Humanised
38	1028	90.6	240	6	ABJ38594	Hepatitis
39	1027.5	90.5	237	3	AAY96289	Human IGF
40	1026	90.4	260	5	ABP41164	Human ova
41	1024	90.2	240	6	ABJ38595	Hepatitis
42	1019.5	89.8	237	3	AAY96301	Human IGF
43	1019	89.8	238	6	ADA47330	TRX1 ligh
44	1019	89.8	238	6	ADA47332	TRX1 ligh
45	1018	89.7	238	2	AAW83032	Anti-Fas

ALIGNMENTS

RESULT 1
AAW95658
ID AAW95658 standard; protein; 218 AA.
XX

AC AAW95658;

DT 08-JUN-1999 (first entry)

DE Mus musculus anti-IgE e25 full length variable light chain.

XX
KW Variable light chain; IgE; antibody; anti-IgE; reduction; prevention;
KW histamine; production; hypersensitivity; allergen; anaphylaxis;
KW atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;
KW eczema; anaphylactic shock; urticaria.

OS Mus musculus.

XX WO9901556-A2.

XX 14-JAN-1999.

PF 30-JUN-1998; 98WO-US013410.

PR 02-JUL-1997; 97US-00887352.

PA (GETH) GENENTECH INC.

PI Lowman HB, Presta LG, Jardieu PM, Lowe J;

XX WPI; 1999-106057/09.

XX Improving affinity of polypeptides, particularly anti-IgE antibodies - by
PT identifying aspartyl residues which undergo isomerisation and
PT substituting alternative residues and screening for affinity against the
target.

XX Disclosure; Page 91-92; 129pp; English.

XX The sequence is that of the full length variable light chain of e25. It
CC was used as part of a method to improve the affinity of anti-IgE
CC antibodies such as e26 and e27. The e26 and e27 antibodies can be used
CC for reducing or preventing IGE mediated production of histamine in a
CC mammal. They can be used for treating a disorder mediated by IGE such as
CC hypersensitivity, atopic allergy, asthma, allergic rhinitis,
CC conjunctivitis, hay fever, eczema, anaphylactic shock and urticaria. The
CC antibodies can also be used for affinity purification, detection and
diagnosis

XX

SQ Sequence 218 AA;
Query Match 100.0%; Score 1135; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 7.2e-57;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDYDGDSDYMNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDYDGDSDYMNWYQKPGKAPKLLIYAASYLE 60

QY 61 GVPSPRFGSGSGTDFLTITSSQLPEDFATYYCQSHEDPYTFGQGTVEIKRTVAAPSVF 120
Db 61 GVPSPRFGSGSGTDFLTITSSQLPEDFATYYCQSHEDPYTFGQGTVEIKRTVAAPSVF 120

QY 121 IFPPSDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDYSL 180

QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 218
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 218

RESULT 2
AAY85200
ID AAY85200 standard; protein; 218 AA.
XX AC AAY85200;
XX DT 29-JUN-2000 (first entry)
XX DE Light chain amino acid sequence of the humanised MaE11 antibody.
XX KW Immunoglobulin E; IgE; anti-human IgE; bispecific antibody; FcEL; FcEH;
KW low affinity binding receptor; high affinity binding receptor; allergy;
KW diagnosis; treatment; histamine release; light chain; prevent; chimeric.
XX OS Mus sp.
OS Homo sapiens.
XX US6037453-A.
XX PD 14-MAR-2000.
XX PF 06-JUN-1995; 95US-00466151.
XX PR 14-AUG-1992; 92WO-US006860.
PR 26-JAN-1994; 94US-00185899.
PR 15-MAR-1995; 95US-00405617.
XX (GETH) GENENTECH INC.
XX PI Presta LG, Jardieu PM;
XX DR WPI; 2000-269913/23.
XX PT New bispecific antibodies, useful for treating immunoglobulin E-mediated
PT disease, binds to IgE, but only when on the low affinity receptor, and to
PT an antigen other than IgE.
XX Claim 14; Fig 3; 48pp; English.
PS This sequence represents the light chain amino acid sequence of a
XX humanised mouse anti-human immunoglobulin E (IgE) antibody. The invention
CC relates to a bispecific antibody that binds specifically to IgE when IgE
CC is bound to its low affinity receptor (FcEL), but does not bind to IgE,
CC when IgE is bound to its high affinity receptor (FcEH). The bispecific
CC antibody comprises an IgE-binding arm with human framework residues of a
CC recipient human antibody and donor murine CDR (complementarity
CC determining region) residues, but with at least one human CDR residue
CC replacing the analogous murine residue. The antibody also comprises an Fv
CC that is specific for a predetermined antigen other than IgE. The
CC antibodies work by displacing bound IgE from its receptor, or via

CC competitive inhibition of its binding. The bispecific antibodies are used
CC for diagnosis, treatment and prevention of allergy and other IgE-mediated
CC diseases, also, when immobilised, for the isolation of FcEL from cells
CC (for research or therapy). The bispecific antibodies of the invention do
CC not cause granulation or release of histamine from mast cells
XX

SQ Sequence 218 AA;
Query Match 100.0%; Score 1135; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 7.2e-57;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDYDGDSDYMNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDYDGDSDYMNWYQKPGKAPKLLIYAASYLE 60

QY 61 GVPSPRFGSGSGTDFLTITSSQLPEDFATYYCQSHEDPYTFGQGTVEIKRTVAAPSVF 120
Db 61 GVPSPRFGSGSGTDFLTITSSQLPEDFATYYCQSHEDPYTFGQGTVEIKRTVAAPSVF 120

QY 121 IFPPSDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDYSL 180

QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 218
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 218

RESULT 3
AAB76947
ID AAB76947 standard; protein; 218 AA.
XX AC AAB76947;
XX DT 17-APR-2001 (first entry)
XX DE Full variable light chain sequence of e25 SEQ ID 13.
XX KW Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
KW antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
KW conjunctivitis; eczema; urticaria; food allergy.
XX OS Synthetic.
XX US6172213-B1.
XX PD 09-JAN-2001.
XX PF 30-JUN-1998; 98US-00109207.
XX PR 02-JUL-1997; 97US-0051554P.
XX (GETH) GENENTECH INC.
XX PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX DR WPI; 2001-122353/13.
XX PT New nucleic acid encoding anti-immunoglobulin E antibody with improved
PT properties, produced by substituting aspartyl residues in unimproved
PT immunoglobulin E prone to isomerization by other residues by affinity
PT maturation with phage display.
XX Disclosure; Fig 2; 87pp; English.
XX This invention relates to a nucleotide sequence encoding an antibody with
CC improved anti-IgE antibody activity. The antibody has improved action due
CC to a process comprising, a) identifying aspartyl residues prone to
CC isomerization in unimproved anti-IgE (immunoglobulin E) antibody; b)
CC substituting alternative residues to create candidate molecules; and c)
CC selecting those candidate molecules which display affinity against the
CC target molecule. Use of the antibody results in antiasthmatic;

anti-allergic; ophthalmological; dermatological and antiinflammatory activity. The antibodies are useful for treating IgE-mediated disorders such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and food allergies. The mutant antibodies produced by the above mentioned nucleic acids may also be used as affinity purification agents and in diagnostic assays for detecting the expression of an antigen of interest in specific cell, tissues or serum. Amino acid sequences AAB76936- AAB76950 represent fragments of anti-IgE antibodies of the invention. Polynucleotide sequence AAF69253 represents an expression plasmid used in the course of the invention, and oligonucleotides AAF69254 - AAF69271 are used in the generation of affinity improved anti-IgE antibodies

Sequence 218 AA;

Residues were selected from MaE11 and inserted or substituted into a human Fab antibody background (Vh region Kabat subgroup III and Vl region kappa subgroup I). A first version, humaE1v1 or version 1 is given below. The affinity of version 1 was assayed and found to be ca. 100 times lower than that of the donor antibody MaE11. Therefore, further modifications in the sequence of version 1 were made. (Updated on 25-MAR-2003 to correct PN field.)

XX	Polypeptide(s) binding to specific Fc epsilon receptors - act as IgE antagonists; useful for treating and preventing IgE-mediated disorders e.g. allergies.
----	---

CC suspected of containing the protein to the antibody and determining the
CC binding of it to the sample. The antibody is also useful for treating
CC cancer, allergic conditions including asthma, LFA-mediated disorders,
CC autoimmune disorders and vasculitis
XX
SQ Sequence 218 AA;
Query Match 98.0%; Score 1112; DB 4; Length 218;
Best Local Similarity 98.2%; Pred. No. 1.4e-55;
Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDRTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
QY 61 GVPFRFSGSGSGTDFTLTISSLPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
Db 61 GVPFRFSGSGSGTDFTLTISSLPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS 180
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS 180
QY 181 STLTLSKADYEKKHVKYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYEKKHVKYACEVTHQGLSSPVTKSFNRGEC 218
RESULT 10
ABU62797
ID ABU62797 standard; protein; 218 AA.
XX
AC ABU62797;
XX
DT 11-SEP-2003 (first entry)
XX
DE E27 anti-immunoglobulin E antibody light chain.
XX
KW Antibody; human immunoglobulin G; autoimmune disorder; E27;
KW anti-immunoglobulin E.
XX
OS Synthetic.
XX
PN US6538124-B1.
XX
PD 25-MAR-2003.
XX
PF 03-OCT-2000; 2000US-00680145.
XX
PR 02-APR-1998; 98US-0080447P.
PR 31-MAR-1999; 99US-00282505.
XX
PA (GETH) GENENTECH INC.
XX
PI Idusogie EE, Presta LG, Mulkerrin MG;
XX
DR WPI; 2003-531086/50.
XX
PT New nucleic acid encodes an antibody variant that binds antigen or an
PT immunoadhesin variant that binds a ligand or receptor, useful for
PT preparing a composition for treating a disorder e.g., autoimmune
PT disorder.
XX
PS Example 1; Fig 4A; 30pp; English.
XX
CC The invention relates to a new isolated nucleic acid that encodes an
CC antibody variant that binds antigen or an immunoadhesin variant that
CC binds a ligand or receptor. The antibody or immunoadhesin variant
CC comprises a human Immunoglobulin G Fc region. The nucleic acid is useful
CC for preparing a composition for treating a disorder e.g. autoimmune
CC disorder. The present sequence represents the amino acid sequence of the
CC E27 anti-immunoglobulin E antibody light chain
XX

SQ Sequence 218 AA;
Query Match 98.0%; Score 1112; DB 6; Length 218;
Best Local Similarity 98.2%; Pred. No. 1.4e-55;
Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDRTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
QY 61 GVPFRFSGSGSGTDFTLTISSLPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
Db 61 GVPFRFSGSGSGTDFTLTISSLPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS 180
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS 180
QY 181 STLTLSKADYEKKHVKYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYEKKHVKYACEVTHQGLSSPVTKSFNRGEC 218
RESULT 11
AAW95664
ID AAW95664 standard; protein; 218 AA.
XX
AC AAW95664;
XX
DT 08-JUN-1999 (first entry)
XX
DE Mus musculus anti-IgE e26 & e27 variable light chain Fab fragment.
XX
KW Variable light Fab fragment; antibody; anti-IgE; reduction; prevention;
KW histamine; production; hypersensitivity; allergen; anaphylaxis;
KW atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;
KW eczema; anaphylactic shock; urticaria; IgE.
XX
OS Mus musculus.
XX
PN WO9901556-A2.
XX
PD 14-JAN-1999.
XX
PF 30-JUN-1998; 98WO-US013410.
XX
PR 02-JUL-1997; 97US-00887352.
XX
PA (GETH) GENENTECH INC.
XX
PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX
DR WPI; 1999-106057/09.
XX
PT Improving affinity of polypeptides, particularly anti-IgE antibodies - by
PT identifying aspartyl residues which undergo isomerisation and
PT substituting alternative residues and screening for affinity against the
PT target.
XX
PS Disclosure; Page 99-100; 129pp; English.
XX
CC The sequence is that of the variable light Fab fragment of e26 and e27.
CC It was used as part of a method to improve the affinity of anti-IgE
CC antibodies such as e26 and e27. The e26 and e27 antibodies can be used
CC for reducing or preventing IgE mediated production of histamine in a
CC mammal. They can be used for treating a disorder mediated by IgE such as
CC hypersensitivity, atopic allergy, asthma, allergic rhinitis,
CC conjunctivitis, hay fever, eczema, anaphylactic shock and urticaria. The
CC antibodies can also be used for affinity purification, detection and
CC diagnosis
XX
SQ Sequence 218 AA;

CC antiallergic; ophthalmological; dermatological and antiinflammatory
CC activity. The antibodies are useful for treating IGE-mediated disorders
CC such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and
CC food allergies. The mutant antibodies produced by the above mentioned
CC nucleic acids may also be used as affinity purification agents and in
CC diagnostic assays for detecting the expression of an antigen of interest
CC in specific cell, tissues or serum. Amino acid sequences AAB76936-
CC AAB76960 represent fragments of anti-IGE antibodies of the invention.
CC Polynucleotide sequence AAF69253 represents an expression plasmid used in
CC the course of the invention, and oligonucleotides AAF69254 - AAF69271 are
CC used in the generation of affinity improved anti-IGE antibodies
XX
SQ Sequence 218 AA;

Query Match 97.7%; Score 1109; DB 4; Length 218;
Best Local Similarity 97.7%; Pred. No. 2.1e-55;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDVRTITCRASQSDYDGSYMNWYQOKPGKAPKLLIYAASYLES 60
Db 1 DIQLTQSPSSLSASVGDVRTITCRASKPVDGEGSYLNWYQOKPGKAPKLLIYAASYLES 60
QY 61 GVPSRFGSGSGTDFTLTISSLOPEDFATYYCQSHEDPYTFGQGTKVEIKRTVAAPSVF 120
Db 61 GVPSRFGSGSGTDFTLTISSLOPEDFATYYCQSHEDPYTFGQGTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS 180
Db 121 IFPPSDEQLKSGTASVVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS 180
QY 181 STLTLISKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLISKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

Search completed: May 13, 2004, 15:45:26
Job time : 33.8137 secs

QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
QY 181 STLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 2
US-08-466-151-9
; Sequence 9, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-9

Query Match 100.0%; Score 1135; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.7e-86;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDRVTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRVTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
QY 61 GVPSRFSGSGGTDFLTITSLQPEDFATYYCQOSHEDPYTFGGTKVEIKRTVAAPSVF 120

Db 61 GVPSRFSGSGGTDFLTITSLQPEDFATYYCQOSHEDPYTFGGTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
QY 181 STLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 3
US-09-109-207C-13
; Sequence 13, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 13
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-13

Query Match 100.0%; Score 1135; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.7e-86;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDRVTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRVTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
QY 61 GVPSRFSGSGGTDFLTITSLQPEDFATYYCQOSHEDPYTFGGTKVEIKRTVAAPSVF 120
Db 61 GVPSRFSGSGGTDFLTITSLQPEDFATYYCQOSHEDPYTFGGTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
QY 181 STLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 4
US-09-296-005-13
; Sequence 13, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 13
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:

NAME/KEY: Artificial
LOCATION: 1-218
OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-296-005-13

Query Match 100.0%; Score 1135; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.7e-86;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDRTTITCRASQSDVDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTTITCRASQSDVDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
QY 61 GVPFRFSGSGSGTDFTLTISSLPEDFATYCCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
Db 61 GVPFRFSGSGSGTDFTLTISSLPEDFATYCCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSL 180
QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 218
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 218

RESULT 5

US-08-466-163B-9

Sequence 9, Application US/08466163B

Patent No. 6329509

GENERAL INFORMATION:

APPLICANT: Jardieu, Paula M.

APPLICANT: Presta, Leonard G.

TITLE OF INVENTION: Immunoglobulin Variants

FILE REFERENCE: P0718P2C1D1

CURRENT APPLICATION NUMBER: US/08/466,163B

CURRENT FILING DATE: 1995-06-06

PRIOR APPLICATION NUMBER: US 08/405,617

PRIOR FILING DATE: 1995-03-15

PRIOR APPLICATION NUMBER: US 08/185,899

PRIOR FILING DATE: 1994-01-26

PRIOR APPLICATION NUMBER: US 07/879,495

PRIOR FILING DATE: 1992-05-07

PRIOR APPLICATION NUMBER: US 07/744,768

PRIOR FILING DATE: 1991-08-14

NUMBER OF SEQ ID NOS: 64

SEQ ID NO 9

LENGTH: 218

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: humanized mae11, version 1, light chain

US-08-466-163B-9

Query Match 100.0%; Score 1135; DB 4; Length 218;

Best Local Similarity 100.0%; Pred. No. 1.7e-86;

Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTTITCRASQSDVDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60

Db 1 DIQLTQSPSSLSASVGDRTTITCRASQSDVDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60

QY 61 GVPFRFSGSGSGTDFTLTISSLPEDFATYCCQSHEDPYTFGQGTKEIKRTVAAPSVF 120

Db 61 GVPFRFSGSGSGTDFTLTISSLPEDFATYCCQSHEDPYTFGQGTKEIKRTVAAPSVF 120

QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSL 180

Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSL 180

QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 218

Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 218

RESULT 6

US-09-920-171-13

Sequence 13, Application US/09920171

Patent No. 6682735

GENERAL INFORMATION:

APPLICANT: Lowman, Henry B.

APPLICANT: Presta, Leonard G.

APPLICANT: Jardieu, Paula M.

APPLICANT: Lowe, John

TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)

FILE REFERENCE: P1123C2US

CURRENT APPLICATION NUMBER: US/09/920,171

CURRENT FILING DATE: 2001-08-01

PRIOR APPLICATION NUMBER: US 08/887,352

PRIOR FILING DATE: 1997-07-02

PRIOR APPLICATION NUMBER: US 09/296,005

PRIOR FILING DATE: 1999-04-21

NUMBER OF SEQ ID NOS: 44

SEQ ID NO 13

LENGTH: 218

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Light chain sequence derived from MAE11

US-09-920-171-13

Query Match 100.0%; Score 1135; DB 4; Length 218;

Best Local Similarity 100.0%; Pred. No. 1.7e-86;

Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTTITCRASQSDVDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60

Db 1 DIQLTQSPSSLSASVGDRTTITCRASQSDVDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60

QY 61 GVPFRFSGSGSGTDFTLTISSLPEDFATYCCQSHEDPYTFGQGTKEIKRTVAAPSVF 120

Db 61 GVPFRFSGSGSGTDFTLTISSLPEDFATYCCQSHEDPYTFGQGTKEIKRTVAAPSVF 120

QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSL 180

Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSL 180

QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 218

Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 218

RESULT 7

US-09-802-096-9

Sequence 9, Application US/09802096

Patent No. 6685939

GENERAL INFORMATION:

APPLICANT: Jardieu, Paula M.

APPLICANT: Presta, Leonard G.

TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)

FILE REFERENCE: P0718P2C3US

CURRENT APPLICATION NUMBER: US/09/802,096

CURRENT FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: US 08/405,617

PRIOR FILING DATE: 1995-03-15

PRIOR APPLICATION NUMBER: US 08/185,899

PRIOR FILING DATE: 1994-01-26

PRIOR APPLICATION NUMBER: PCT/US92/06860

PRIOR FILING DATE: 1992-08-14

PRIOR APPLICATION NUMBER: US 07/879,495

PRIOR FILING DATE: 1992-05-07

PRIOR APPLICATION NUMBER: US 07/744,768

PRIOR FILING DATE: 1991-08-14

NUMBER OF SEQ ID NOS: 64

SEQ ID NO 9

LENGTH: 218


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; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mae11, version 1, light chain
US-09-802-096-9

Query Match      100.0%; Score 1135; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.7e-86;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITTCRASQSDYDGDSDYNNWYQOKPGKAPKLLIYAASYLE 60
   |||||||
Db 1 DIQLTQSPSSLSASVGDRTVITTCRASQSDYDGDSDYNNWYQOKPGKAPKLLIYAASYLE 60
   |||||||

QY 61 GVPSPRFGSGSGTDFTLTISSLOPEDFATYYCQOSHEDPYTFGQGTKEIKRTVAAPSVF 120
   |||||||
Db 61 GVPSPRFGSGSGTDFTLTISSLOPEDFATYYCQOSHEDPYTFGQGTKEIKRTVAAPSVF 120
   |||||||

QY 121 IFPPSDEQLKSGTASVCLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDYSL 180
   |||||||
Db 121 IFPPSDEQLKSGTASVCLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDYSL 180
   |||||||

QY 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
   |||||||
Db 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
   |||||||

RESULT 8
US-09-282-505-1
; Sequence 1, Application US/09282505A
; Patent No. 6194551
; GENERAL INFORMATION:
; APPLICANT: Esohe Ekinaduese Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R1
; CURRENT APPLICATION NUMBER: US/09/282,505A
; CURRENT FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-218
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6194551
US-09-282-505-1

Query Match      98.0%; Score 1112; DB 3; Length 218;
Best Local Similarity 98.2%; Pred. No. 1.4e-84;
Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITTCRASQSDYDGDSDYNNWYQOKPGKAPKLLIYAASYLE 60
   |||||||
Db 1 DIQLTQSPSSLSASVGDRTVITTCRASQSDYDGDSDYNNWYQOKPGKAPKLLIYAASYLE 60
   |||||||

QY 61 GVPSPRFGSGSGTDFTLTISSLOPEDFATYYCQOSHEDPYTFGQGTKEIKRTVAAPSVF 120
   |||||||
Db 61 GVPSPRFGSGSGTDFTLTISSLOPEDFATYYCQOSHEDPYTFGQGTKEIKRTVAAPSVF 120
   |||||||

QY 121 IFPPSDEQLKSGTASVCLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDYSL 180
   |||||||
Db 121 IFPPSDEQLKSGTASVCLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDYSL 180
   |||||||

QY 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
   |||||||
Db 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
   |||||||

RESULT 9
US-09-054-255-1
; Sequence 1, Application US/09054255
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; Patent No. 6242195
; GENERAL INFORMATION:
; APPLICANT: Esohe Ekinaduese Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266
; CURRENT APPLICATION NUMBER: US/09/054,255
; CURRENT FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: E27 anti-IgE antibody light chain
US-09-054-255-1

Query Match      98.0%; Score 1112; DB 3; Length 218;
Best Local Similarity 98.2%; Pred. No. 1.4e-84;
Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITTCRASQSDYDGDSDYNNWYQOKPGKAPKLLIYAASYLE 60
   |||||||
Db 1 DIQLTQSPSSLSASVGDRTVITTCRASQSDYDGDSDYNNWYQOKPGKAPKLLIYAASYLE 60
   |||||||

QY 61 GVPSPRFGSGSGTDFTLTISSLOPEDFATYYCQOSHEDPYTFGQGTKEIKRTVAAPSVF 120
   |||||||
Db 61 GVPSPRFGSGSGTDFTLTISSLOPEDFATYYCQOSHEDPYTFGQGTKEIKRTVAAPSVF 120
   |||||||

QY 121 IFPPSDEQLKSGTASVCLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDYSL 180
   |||||||
Db 121 IFPPSDEQLKSGTASVCLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDYSL 180
   |||||||

QY 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
   |||||||
Db 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
   |||||||

RESULT 10
US-09-282-846-1
; Sequence 1, Application US/09282846
; Patent No. 6528624
; GENERAL INFORMATION:
; APPLICANT: Esohe Ekinaduese Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R2
; CURRENT APPLICATION NUMBER: US/09/282,846
; CURRENT FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-218
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6528624
US-09-282-846-1

Query Match      98.0%; Score 1112; DB 4; Length 218;
Best Local Similarity 98.2%; Pred. No. 1.4e-84;
Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITTCRASQSDYDGDSDYNNWYQOKPGKAPKLLIYAASYLE 60
   |||||||
Db 1 DIQLTQSPSSLSASVGDRTVITTCRASQSDYDGDSDYNNWYQOKPGKAPKLLIYAASYLE 60
   |||||||

QY 61 GVPSPRFGSGSGTDFTLTISSLOPEDFATYYCQOSHEDPYTFGQGTKEIKRTVAAPSVF 120
   |||||||
Db 61 GVPSPRFGSGSGTDFTLTISSLOPEDFATYYCQOSHEDPYTFGQGTKEIKRTVAAPSVF 120
   |||||||

QY 121 IFPPSDEQLKSGTASVCLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDYSL 180
   |||||||
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Db 121 IFPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180

Qy 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218

Db 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 11

US-09-680-145-1

; Sequence 1, Application US/09680145

; Patent No. 6538124

; GENERAL INFORMATION:

; APPLICANT: Esche Ekinaduese Idusogie et al.

; TITLE OF INVENTION: Polypeptide Variants

; FILE REFERENCE: P1266R1

; CURRENT APPLICATION NUMBER: US/09/680,145

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 09/282,505

; PRIOR FILING DATE: 1999-03-13

; NUMBER OF SEQ ID NOS: 2

; SEQ ID NO 1

; LENGTH: 218

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: Artificial Sequence

; LOCATION: 1-218

; OTHER INFORMATION: Sequence is completely synthesized

; Patent No. 6538124

US-09-680-145-1

Query Match 98.0%; Score 1112; DB 4; Length 218;

Best Local Similarity 98.2%; Pred. No. 1.4e-84;

Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60

Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGEGSDYNNWYQKPGKAPKLLIYAASYLE 60

Qy 61 GVPFRFSGSGSGTDFTLTISLQPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120

Db 61 GVPFRFSGSGSGTDFTLTISLQPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120

Qy 121 IFPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180

Db 121 IFPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180

Qy 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218

Db 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 12

US-08-887-352B-15

; Sequence 15, Application US/08887352B

; Patent No. 5994511

; GENERAL INFORMATION:

; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe

; TITLE OF INVENTION: Improved Anti-Ige Antibodies and Method of

; TITLE OF INVENTION: Improving Polypeptides

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/887,352B

; FILING DATE: 03-Jul-1997

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Svoboda, Craig G.

; REGISTRATION NUMBER: 39,044

; REFERENCE/DOCKET NUMBER: P1123

; TELEPHONE: 650/225-1489

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 15:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 218 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-08-887-352B-15

Query Match 97.7%; Score 1109; DB 2; Length 218;

Best Local Similarity 97.7%; Pred. No. 2.4e-84;

Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60

Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGEGSDYNNWYQKPGKAPKLLIYAASYLE 60

Qy 61 GVPFRFSGSGSGTDFTLTISLQPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120

Db 61 GVPFRFSGSGSGTDFTLTISLQPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120

Qy 121 IFPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180

Db 121 IFPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180

Qy 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218

Db 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 13

US-08-887-352B-17

; Sequence 17, Application US/08887352B

; Patent No. 5994511

; GENERAL INFORMATION:

; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe

; TITLE OF INVENTION: Improved Anti-Ige Antibodies and Method of

; TITLE OF INVENTION: Improving Polypeptides

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/887,352B

; FILING DATE: 03-Jul-1997

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Svoboda, Craig G.

; REGISTRATION NUMBER: 39,044

; REFERENCE/DOCKET NUMBER: P1123

; TELEPHONE: 650/225-1489

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 17:

; SEQUENCE CHARACTERISTICS:

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; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-17

Query Match
Best Local Similarity 97.7%; Score 1109; DB 2; Length 218;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVTITCRASQSDYDGDSDYNNWYQKPKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTVTITCRASKPVDGEGDSYLNWYQKPKAPKLLIYAASYLE 60

QY 61 GVPFRFSGSGSGTDFTLTISSLOPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
Db 61 GVPFRFSGSGSGTDFTLTISSLOPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120

QY 121 IFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180

QY 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNREGC 218
Db 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNREGC 218

RESULT 14
US-08-887-352B-19
; Sequence 19, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-19

Query Match
Best Local Similarity 97.7%; Score 1109; DB 2; Length 218;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVTITCRASQSDYDGDSDYNNWYQKPKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTVTITCRASKPVDGEGDSYLNWYQKPKAPKLLIYAASYLE 60
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QY 61 GVPFRFSGSGSGTDFTLTISSLOPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
Db 61 GVPFRFSGSGSGTDFTLTISSLOPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120

QY 121 IFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180

QY 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNREGC 218
Db 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNREGC 218

RESULT 15
US-08-887-352B-24
; Sequence 24, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-24

Query Match
Best Local Similarity 97.7%; Score 1109; DB 2; Length 218;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVTITCRASQSDYDGDSDYNNWYQKPKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTVTITCRASKPVDGEGDSYLNWYQKPKAPKLLIYAASYLE 60

QY 61 GVPFRFSGSGSGTDFTLTISSLOPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
Db 61 GVPFRFSGSGSGTDFTLTISSLOPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120

QY 121 IFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180

QY 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNREGC 218
Db 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNREGC 218
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Search completed: May 13, 2004, 15:48:48
Job time : 11.7213 secs


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; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 13
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-920-171-13

Query Match      100.0%; Score 1135; DB 9; Length 218;
Best Local Similarity 100.0%; Pred. No. 9e-64;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRTTITCRASQSVDDYDGDSDYMNWYQQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTTITCRASQSVDDYDGDSDYMNWYQQKPGKAPKLLIYAASYLE 60
Qy 61 GVPSRFSGSGSGTDFTLTITSSLPEDFATYYCQQSHEDPYTFGQGTKEIKRTVAAPSVF 120
Db 61 GVPSRFSGSGSGTDFTLTITSSLPEDFATYYCQQSHEDPYTFGQGTKEIKRTVAAPSVF 120
Qy 121 IFPPSDEQLKSGTASVWCLLNFFYPREAKVQWVDNALQSGNSQESVTEQDSKDSYSL 180
Db 121 IFPPSDEQLKSGTASVWCLLNFFYPREAKVQWVDNALQSGNSQESVTEQDSKDSYSL 180
Qy 181 STLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 218
Db 181 STLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 218

RESULT 4
US-09-925-179-9
; Sequence 9, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 9
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mae11, version 1, light chain
US-09-925-179-9

Query Match      100.0%; Score 1135; DB 10; Length 218;
Best Local Similarity 100.0%; Pred. No. 9e-64;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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QY 1 DIQLTQSPSSLSASVGDRTTITCRASQSDYDGDSDYNNWYQQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTTITCRASQSDYDGDSDYNNWYQQKPGKAPKLLIYAASYLE 60
QY 61 GVPFRFSGSGSGTDFTLTISSLOPEDFATYCCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
Db 61 GVPFRFSGSGSGTDFTLTISSLOPEDFATYCCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
Db 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 5
US-10-113-996-13
; Sequence 13, Application US/10113996
; Publication No. US20030149244A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies
; FILE REFERENCE: P1123C3US
; CURRENT APPLICATION NUMBER: US/10/113,996
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 09/920,171
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 13
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-10-113-996-13

Query Match 100.0%; Score 1135; DB 14; Length 218;
Best Local Similarity 100.0%; Pred. No. 9e-64;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDRTTITCRASQSDYDGDSDYNNWYQQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTTITCRASQSDYDGDSDYNNWYQQKPGKAPKLLIYAASYLE 60
QY 61 GVPFRFSGSGSGTDFTLTISSLOPEDFATYCCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
Db 61 GVPFRFSGSGSGTDFTLTISSLOPEDFATYCCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
Db 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 6
US-09-925-179-67
; Sequence 67, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.

; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 67
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Full-length light chain sequence corresponding to F(ab)9 of Tabl
US-09-925-179-67

Query Match 98.7%; Score 1120; DB 10; Length 218;
Best Local Similarity 97.7%; Pred. No. 7.8e-63;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDRTTITCRASQSDYDGDSDYNNWYQQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTTITCRASQSDYDGDSDYNNWYQQKPGKAPKLLIYAASYLE 60
QY 61 GVPFRFSGSGSGTDFTLTISSLOPEDFATYCCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
Db 61 GVPFRFSGSGSGTDFTLTISSLOPEDFATYCCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
Db 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 7
US-09-792-938-1
; Sequence 1, Application US/09792938
; Publication No. US20030166868A1
; GENERAL INFORMATION:
; APPLICANT: Esche Ekinaduese Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R1
; CURRENT APPLICATION NUMBER: US/09/792,938
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 09/282,505
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-218
; OTHER INFORMATION: Sequence is completely synthesized
US-09-792-938-1

Query Match 98.0%; Score 1112; DB 10; Length 218;
Best Local Similarity 98.2%; Pred. No. 2.5e-62;
Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 121 IFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
QY 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 11
US-09-920-171-19
; Sequence 19, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 19
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain F(ab) sequence derived from MAE11
US-09-920-171-19

Query Match 97.7%; Score 1109; DB 9; Length 218;
Best Local Similarity 97.7%; Pred. No. 3.8e-62;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDRTTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
QY 61 GVPSPSGSGSGTDFTLTISSLPEDFATYCCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
Db 61 GVPSPSGSGSGTDFTLTISSLPEDFATYCCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
QY 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 12
US-09-920-171-24
; Sequence 24, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005

; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 24
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain F(ab)'2 sequence derived from MAE11
US-09-920-171-24

Query Match 97.7%; Score 1109; DB 9; Length 218;
Best Local Similarity 97.7%; Pred. No. 3.8e-62;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDRTTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
QY 61 GVPSPSGSGSGTDFTLTISSLPEDFATYCCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
Db 61 GVPSPSGSGSGTDFTLTISSLPEDFATYCCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
QY 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 13
US-10-113-996-15
; Sequence 15, Application US/10113996
; Publication No. US20030149244A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies
; FILE REFERENCE: P1123C3US
; CURRENT APPLICATION NUMBER: US/10/113,996
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 09/920,171
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 15
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-10-113-996-15

Query Match 97.7%; Score 1109; DB 14; Length 218;
Best Local Similarity 97.7%; Pred. No. 3.8e-62;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDRTTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
QY 61 GVPSPSGSGSGTDFTLTISSLPEDFATYCCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
Db 61 GVPSPSGSGSGTDFTLTISSLPEDFATYCCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180

Db 121 IFPPSDEQLKSGTASVVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDYSTYLS 180
Qy 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 14
US-10-113-996-17
; Sequence 17, Application US/10113996
; Publication No. US20030149244A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies
; FILE REFERENCE: P1123C3US
; CURRENT APPLICATION NUMBER: US/10/113,996
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 09/920,171
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 17
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-10-113-996-17

Query Match 97.7%; Score 1109; DB 14; Length 218;
Best Local Similarity 97.7%; Pred. No. 3.8e-62;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 DIQLTQSPSSLSASVGDRTTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Qy 61 GVPSPFSGSGGTDFTLTISSLPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
Db 61 GVPSPFSGSGGTDFTLTISSLPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
Qy 121 IFPPSDEQLKSGTASVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDYSTYLS 180
Db 121 IFPPSDEQLKSGTASVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDYSTYLS 180
Qy 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 15
US-10-113-996-19
; Sequence 19, Application US/10113996
; Publication No. US20030149244A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies
; FILE REFERENCE: P1123C3US
; CURRENT APPLICATION NUMBER: US/10/113,996
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21

; PRIOR APPLICATION NUMBER: US 09/920,171
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 19
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain F(ab) sequence derived from MAE11
US-10-113-996-19

Query Match 97.7%; Score 1109; DB 14; Length 218;
Best Local Similarity 97.7%; Pred. No. 3.8e-62;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 DIQLTQSPSSLSASVGDRTTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Qy 61 GVPSPFSGSGGTDFTLTISSLPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
Db 61 GVPSPFSGSGGTDFTLTISSLPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
Qy 121 IFPPSDEQLKSGTASVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDYSTYLS 180
Db 121 IFPPSDEQLKSGTASVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDYSTYLS 180
Qy 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218

Search completed: May 13, 2004, 15:56:57
Job time : 26.3413 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:38:23 ; Search time 9.09687 Seconds
(without alignments)
2305.161 Million cell updates/sec

Title: US-09-925-179-9
Perfect score: 1135
Sequence: 1 DIQLTQSPSSLASVGDVRT.....EVTHQGLSSPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	942.5	83.0	215	2 JE0242	Ig kappa chain NIG
2	917.5	80.8	215	2 JE0244	Ig kappa chain NIG
3	892.5	78.6	215	2 JE0243	Ig kappa chain NIG
4	883	77.8	216	2 JE0241	Ig kappa chain Am3
5	875.5	77.1	215	2 A23746	Ig kappa chain V-I
6	759	66.9	240	2 S06084	Ig kappa chain pre
7	739	65.1	218	2 S68241	Ig kappa chain V r
8	737	64.9	218	2 JC5810	monoclonal antibod
9	727	64.1	230	2 S33161	Ig kappa chain - s
10	723	63.7	220	2 A31790	Ig kappa chain V r
11	718	63.3	234	2 S14237	Ig kappa chain pre
12	716	63.1	234	2 S01320	Ig kappa chain pre
13	712	62.7	210	2 A56169	Ig kappa chain V r
14	699	61.6	214	2 S68212	Ig kappa chain (Ma
15	698.5	61.5	219	2 S38865	Ig kappa chain - m
16	694.5	61.2	217	2 S42772	Ig kappa chain - m
17	693.5	61.1	225	2 S37484	Ig kappa chain - m
18	692.5	61.0	219	2 PC4203	Ig kappa chain (mo
19	689.5	60.7	219	2 S52028	Ig kappa chain - m
20	687.5	60.6	235	2 S25058	Ig kappa chain - m
21	683.5	60.2	219	2 S16112	Ig kappa chain V r
22	670.5	59.1	225	2 JL0029	Ig kappa chain pre
23	608	53.6	135	2 S52059	JC-kappa protein -
24	596	52.5	178	2 PT0219	Ig kappa chain V-C
25	563.5	49.6	229	2 A20969	Ig kappa chain pre
26	548	48.3	106	1 K3HU	Ig kappa chain C r
27	535.5	47.2	197	2 S29593	Ig kappa chain (WM
28	534.5	47.1	238	2 A49633	Ig lambda-like cha
29	513	45.2	99	2 A37927	Ig kappa chain C r

30	507	44.7	99	2 S26653	Ig kappa chain C r
31	505	44.5	127	2 S40367	Ig kappa chain V-J
32	498	43.9	233	2 S29577	Ig light chain - r
33	494	43.5	123	2 S40331	Ig kappa chain - h
34	493	43.4	108	2 B49047	Ig kappa chain V r
35	482	42.5	109	2 S31998	Ig kappa chain - h
36	481	42.4	141	2 A49134	Ig kappa chain V-I
37	478	42.1	108	2 S44122	Ig kappa chain V r
38	477	42.0	144	2 PL0106	Ig kappa chain pre
39	476	41.9	108	2 S47182	Ig kappa chain - h
40	475	41.9	139	2 S40365	Ig kappa chain - h
41	472	41.6	120	2 S46370	Ig kappa chain V-J
42	471	41.5	108	1 K1HUHU	Ig kappa chain V-I
43	471	41.5	109	2 S31981	Ig kappa chain - h
44	470	41.4	132	2 S40334	Ig kappa chain - h
45	469.5	41.4	125	2 S40315	Ig kappa chain - h

ALIGNMENTS

RESULT 1

JE0242
Ig kappa chain NIG26 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0242
R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, submitted to JIPID, November 1998
A;Description: Structure relationship of kappatype light chains with AL amyloidosis: Mu
A;Reference number: JE0241
A;Accession: JE0242
A;Molecule type: protein
A;Residues: 1-215 <Ali>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 83.0%; Score 942.5; DB 2; Length 215;
Best Local Similarity 83.5%; Pred. No. 1.4e-55;
Matches 182; Conservative 13; Mismatches 20; Indels 3; Gaps 1;

QY	1	DIQLTQSPSSLASVGDVRTITITCRASQSDYDGDSDYNNWYQQPKAPKLLIYAASYLE	60
Db	1	EIVLTQSPGTLSPGERATLSCRASQSV---SNNYLAWYQQKPGQAPSLIIYDASSRAT	57
QY	61	GVPSRFSGSGSGTDFTLTITSSLPQEDFATYYCQQSHEDPYTFGQGTKEIKRTVAAPSVF	120
Db	58	GIPDRFSGSGSGTDFTLTISGLEPEDFAVYYCQYDRPPWTFGQGTKEIKRTVAAPSVF	117
QY	121	IFPPSDEQLKSGTASVWCLLNFPYFPEAKVQWKVDNALQSGNSQESVTEQDSKDSYSL	180
Db	118	IFPPSDEQLKSGTASVWCLLNFPYFPEAKVQWKVDNALQSGNSQESVTEQDSKDSYSL	177
QY	181	STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC	218
Db	178	STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC	215

RESULT 2

JE0244
Ig kappa chain NIG2 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0244
R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; submitted to JIPID, November 1998
A;Description: A new subgroup of k type light chains (VKV) identified in cases of AL am
A;Reference number: JE0243
A;Accession: JE0244
A;Molecule type: protein
A;Residues: 1-215 <Ali>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

F:16-92/Domain: immunoglobulin homology <IMM>

```
Query Match      80.8%; Score 917.5; DB 2; Length 215;
Best Local Similarity 82.6%; Pred. No. 6.2e-54;
Matches 181; Conservative 14; Mismatches 19; Indels 5; Gaps 2;
```

Qy	1	DIQLTQSPSLSASVGDRTVITICRASQSVDYDGDSDVMNVYQQKPGKAPKLLIYAASYLES	60
	:	: : : : : : : : : : : : : : : : :	:
Dd	1	EVVLTTQSPATLTVSVSGERATLSCRASQSV---HSNLAWYQQKPGQAPRLLIYRASTRAT	56
Qy	61	GVPSRFSGSGGTDFLTITSSLOPEDFATYYCQQSHEDPYTFGQGTKVEIKRTVAAPSV	119
	:	: : : : : : : : : : : : : : : : :	:
Dd	57	GIPARFSGSGGTDFILTITSSLOSEDFALYYCQQYNTPWPLTFGGTKVEIKRTVAAPSV	116
Qy	120	FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL	179
	:	: : : : : : : : : : : : : : : : :	:
Dd	117	FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL	176
Qy	180	SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	218
	:	: : : : : : : : : : : : : : : : :	:
Dd	177	SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	215

```

RESULT 3
JEO243
Ig kappa chain NIG93 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JEO243
R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T
submitted to JIPID, November 1998
A;Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy
A;Reference number: JEO243
A;Accession: JEO243
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

```

	Query Match	78.6%;	Score 892.5;	DB 2;	Length 215;	
	Best Local Similarity	81.3%;	Pred. No. 2.8e-52;			
	Matches 178; Conservative	16;	Mismatches 20;	Indels 5;	Gaps 2	

QY	1	DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSYMWNWYQQKPGKAPKLLIYAASYLES	60
	:	: : : : : : : : : : : : : : : : :	:
DB	1	EIVMTQSPATLSVSPGERATLSCRASQSV---ATNVVWYMQKLQGAPRLLIYDASTRAT	56
QY	61	GVPSRFGSGSGTDFTLTISSLQPEDFAFYQCQSHEDPYTFGQGTKVEIK-RTVAAPS	119
	:	: : : : : : : : : : : : : : : :	:
DB	57	GVPAFPFGSGSGTEFTLTISSLQSEDFAIYCQHNNAWPPTFGQTKVKETKRRTVAAPS	116
QY	120	FIFPSPDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS	179
	:	: : : : : : : : : : : : : : : :	:
DB	117	FIFPSPDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS	176
QY	180	SSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC	218
	:	: : : : : : : : : : : : : : : :	:
DB	177	SSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC	215

```

RESULT 4
JE0241
IG kappa chain Am37 precursor - human
C/Species: Homo sapiens (man)
C/Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C/Accession: JE0241
R/Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.
submitted to JIPID, November 1998
A/Description: Structure relationship of kappa type light chains with AL amyloidosis: Mu
A/Reference number: JE0241
A/Accession: JE0241
A/Molecule type: protein
A/Residues: 1-216 <ALI>
C/Superfamily: immunoglobulin V region; immunoglobulin homology

```

	Query Match	77.1%;	Score 875.5;	DB 2;	Length 215;
	Best Local Similarity	81.1%;	Pred. No. 3.7e-51;		
	Matches 176;	Conservative 13;	Mismatches 25;	Indels 3;	Gaps 1
QY	1	D I Q L T Q S P S S L S A S V G D R V T I T C R A S Q S V D Y D G D S Y M N W Y Q Q K P K A P K L L I Y A A S Y L S	60		
		: :			
Db	1	E I V L T Q S P A T L S L S P G E R A T L S G G A S Q S V - - S S N Y L A W Y Q Q K P Q A P R L L I Y D A S S R A T	57		
QY	61	G V P S R F S G S G S G T D F T L T I S S L O P E D F A T Y Y C Q Q S H E D P Y T F G Q G T K V E I K R T V A A P S V F	120		
		: :			
Db	58	G I P D R F S G S G S G T D F T L T I S R L E B E D F A V Y Y G Q Y G S S P L T F G G G T K V E I K R T V A A P S V F	117		
QY	121	I F P S D E Q L K S G T A S V V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S	180		
		: :			
Db	118	I F P S D E Q L K S G T A S V V G L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S	177		
QY	181	S T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N R G E	217		
		: :			
Db	178	S T L T L S K A D Y E K H K V Y A G E V T H Q G L S S P V T K S F N R G E	214		

RESULT 6
S06084
Ig kappa chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C:Accession: S06084
R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A:Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa
A:Reference number: S06084; MUID:90016888; PMID:2508067
A:Accession: S06084

QY 121 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 133 LFKPSEEQLRTGTSVVCLVNDYFPKDINVKVKGVDGVTQNSNFQNSFTDQDSKKSTYSL 192
QY 181 STLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNREGC 218
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 193 STLTLSSEYQSHNAYACEVSHKSLPTALVKSFNKNEC 230
RESULT 10
A31790
Ig kappa chain V region (17/9) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C:Accession: A31790
R;Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1988
A;Title: Preliminary crystallographic data, primary sequence, and binding data for an an
A;Reference number: A92686; MUID:89034213; PMID:3182835
A;Accession: A31790
A;Molecule type: mRNA
A;Residues: 1-220 <SCH>
A;Cross-references: GB:M23626; GB:J04061; NID:G533234; PIDN:AAA39162.1; PID:G533235
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>
Query Match 63.7%; Score 723; DB 2; Length 220;
Best Local Similarity 61.4%; Pred. No. 4.5e-41;
Matches 135; Conservative 34; Mismatches 49; Indels 2; Gaps 1;
QY 1 DIQLTQSPSSLSASVGDRTVTITCRASQSDYDG--DSYMNWYQKPGKAPKLLIYAASYL 58
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIVMTQSPSSLTVTAGKVTMSCTSSQSLFNSGKQKNLYTWYQKPGQPPKVLIIWASTR 60
QY 59 ESGVPSRFSGSGTDFTLTISSLPQEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPS 118
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ESGVPDRFTGSGTDFTLTISSVQAE DLAVYYCQNDYSNPLTFGGTKLEKRAADAAPT 120
QY 119 VFIFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 178
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 VSIFPPSDEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDYSL 180
QY 179 LSSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNREGC 218
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 MSSTLTLTCKDEYERHNSYTCETHKSTSTSPIVKSFNRNEC 220
RESULT 11
S14237
Ig kappa chain precursor (15C5) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S14237
R;Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D.
Eur. J. Biochem. 192, 767-775, 1990
A;Title: Construction and characterization of a recombinant murine monoclonal antibody d
A;Reference number: S14236; MUID:91006173; PMID:2209622
A;Accession: S14237
A;Molecule type: mRNA
A;Residues: 1-234 <VAN>
A;Cross-references: EMBL:X56394; NID:G51622; PIDN:CAA39805.1; PID:G51623
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>
Query Match 63.3%; Score 718; DB 2; Length 234;
Best Local Similarity 61.5%; Pred. No. 1e-40;
Matches 134; Conservative 35; Mismatches 45; Indels 4; Gaps 1;
QY 1 DIQLTQSPSSLSASVGDRTVTITCRASQSDYDGDSYMNWYQKPGKAPKLLIYAASYLES 60
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 21 DIKMTQSPSSMYASLGERTVTCTCKASQDI----NSYLSWIQQKPGKSPKTLIYRGNRLVA 76
QY 61 GVPFRFSGSGSGTDFTLTISSLPQEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPS 120
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 77 GVPFRFSGSGSGQDYSLTISLEYEDGVVYCLRYDEFFFTFGSGTKLEIKRAADAAPT 136
QY 121 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 137 IFPPSDEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDYSL 196
QY 181 STLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNREGC 218
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 197 STLTLTCKDEYERHNSYTCETHKSTSTSPIVKSFNRNEC 234
RESULT 12
S01320
Ig kappa chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 21-Jan-2000
C:Accession: S01320
R;de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed
A;Reference number: S01320; MUID:88329081; PMID:3138116
A;Accession: S01320
A;Molecule type: mRNA
A;Residues: 1-234 <DE1>
A;Cross-references: EMBL:X13187; NID:G51784; PIDN:CAA31579.1; PID:G51785
A;Note: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-234/Product: Ig kappa chain #status predicted <MAT>
F;36-110/Domain: immunoglobulin homology <IMM>
Query Match 63.1%; Score 716; DB 2; Length 234;
Best Local Similarity 61.4%; Pred. No. 1.4e-40;
Matches 135; Conservative 33; Mismatches 44; Indels 8; Gaps 2;
QY 1 DIQLTQSPSSLSASVGDRTVTITCRASQSDYDGDSYMN--WYQKPGKAPKLLIYAASYL 58
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 21 DIQMTQSPASLSVSGESVTITCRASENI-----YSNLAWYQKQKSPQLLVYVATKL 74
QY 59 ESGVPSRFSGSGSGTDFTLTISSLPQEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPS 118
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 75 VDGVPFRFSGSGSGTQYSLKINSLSQSEDFGSYYCQHFWDTPFTFGSGTKLEMKRAADAAPT 134
QY 119 VFIFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 178
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 135 VSIFPPSDEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDYSL 194
QY 179 LSSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNREGC 218
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 195 MSSTLTLTCKDEYERHNSYTCETHKSTSTSPIVKSFNRNEC 234
RESULT 13
A56169
Ig kappa chain V region (clone 23.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 11-Jan-2000
C:Accession: A56169
R;Monfardini, C.; Kieber-Emmons, T.; VonFeltdt, J.M.; O'Malley, B.; Rosenbaum, H.; Godil
J. Biol. Chem. 270, 6628-6638, 1995
A;Title: Recombinant antibodies in bioactive peptide design.
A;Reference number: A56169; MUID:95204454; PMID:7896802
A;Accession: A56169
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-210 <MON>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:10:58 ; Search time 6.82265 Seconds
(without alignments)
1663.765 Million cell updates/sec

Title: US-09-925-179-9
Perfect score: 1135
Sequence: 1 DIQLTQSPSSLASVGDRT.....EVTHQGLSSPVTKSPNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	548	48.3	106	1 KAC HUMAN	P01834 homo sapien
2	471	41.5	108	1 KV1H HUMAN	P01600 homo sapien
3	467	41.1	111	1 KV3M MOUSE	P01665 mus musculu
4	463	40.8	108	1 KV1E HUMAN	P01597 homo sapien
5	462	40.7	111	1 KV3O MOUSE	P01667 mus musculu
6	460	40.5	111	1 KV3N MOUSE	P01666 mus musculu
7	460	40.5	129	1 KV1W HUMAN	P04431 homo sapien
8	459	40.4	111	1 KV3Q MOUSE	P01669 mus musculu
9	455	40.1	111	1 KV3L MOUSE	P01664 mus musculu
10	454	40.0	108	1 KV1V HUMAN	P04430 homo sapien
11	452	39.8	108	1 KV1N HUMAN	P01606 homo sapien
12	448	39.5	108	1 KV1B HUMAN	P01594 homo sapien
13	448	39.5	108	1 KV1M HUMAN	P01605 homo sapien
14	446.5	39.3	110	1 KV3P MOUSE	P01668 mus musculu
15	444	39.1	108	1 KV1K HUMAN	P01603 homo sapien
16	444	39.1	108	1 KV1S HUMAN	P01611 homo sapien
17	443	39.0	108	1 KV1F HUMAN	P01598 homo sapien
18	443	39.0	108	1 KV1O HUMAN	P01607 homo sapien
19	442	38.9	108	1 KV1G HUMAN	P01599 homo sapien
20	441	38.9	108	1 KV1Y HUMAN	P03362 homo sapien
21	439	38.7	108	1 KV1R HUMAN	P01610 homo sapien
22	438	38.6	108	1 KV1P HUMAN	P01608 homo sapien
23	437	38.5	108	1 KV1L HUMAN	P01604 homo sapien
24	431	38.0	108	1 KV1A HUMAN	P01593 homo sapien
25	430.5	37.9	109	1 KV1T HUMAN	P01612 homo sapien
26	429.5	37.8	107	1 KV1D HUMAN	P01596 homo sapien
27	429	37.8	111	1 KV3H MOUSE	P01660 mus musculu
28	425	37.4	108	1 KV1Q HUMAN	P01609 homo sapien
29	423	37.3	108	1 KV1C HUMAN	P01595 homo sapien
30	420	37.0	111	1 KV3J MOUSE	P01662 mus musculu
31	419	36.9	129	1 KV1X HUMAN	P04432 homo sapien
32	415	36.6	131	1 KV3I MOUSE	P01661 mus musculu
33	411	36.2	111	1 KV3K MOUSE	P01663 mus musculu

34	410	36.1	114	1 KV4A HUMAN	P01625 homo sapien
35	410	36.1	134	1 KV4C HUMAN	P06314 homo sapien
36	404	35.6	111	1 KV3R MOUSE	P01670 mus musculu
37	404	35.6	111	1 KV3S MOUSE	P01671 mus musculu
38	404	35.6	112	1 KV1U HUMAN	P01613 homo sapien
39	404	35.6	112	1 KV3G MOUSE	P01659 mus musculu
40	404	35.6	132	1 KV3F MOUSE	P01658 mus musculu
41	402	35.4	117	1 KV1J HUMAN	P01602 homo sapien
42	400.5	35.3	129	1 KV3L HUMAN	P18135 homo sapien
43	399.5	35.2	129	1 KV3M HUMAN	P18136 homo sapien
44	399	35.2	111	1 KV3U MOUSE	P01673 mus musculu
45	396.5	34.9	109	1 KV3B HUMAN	P01620 homo sapien

ALIGNMENTS

RESULT 1
KAC HUMAN
ID_ KAC HUMAN STANDARD; PRT; 106 AA.
AC P01834;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ig kappa chain C region.
GN IGKC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (MYELOMA PROTEIN EU).
RX MEDLINE=71064023; PubMed=5489770;
RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";
RL Biochemistry 9:3155-3161(1970).
RN [2]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;
RA Gail W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
RN [3]
RP SEQUENCE (BENCE-JONES PROTEIN TI).
RX MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=81042304; PubMed=6775818;
RA Hieter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;
RT "Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments.";
RL Cell 22:197-207(1980).
RN [5]
RP SEQUENCE (BENCE-JONES PROTEIN ROY).
RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;
RL (In) Franek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).
RN [6]
RP SEQUENCE (BENCE-JONES PROTEIN CUM).
RX MEDLINE=68242259; PubMed=5586923;
RA Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";

RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [7]
RP SEQUENCE (BENCE-JONES PROTEIN AG).
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3550-3560(1969).
RN [8]
RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
RX MEDLINE=70201507; PubMed=547531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains.";
RL Science 169:56-59(1970).
RN [9]
RP SEQUENCE OF 1-33; 38-41 AND 62-80.
RX TISSUE=Abdominal adipose tissue;
MEDLINE=98249779; PubMed=9588180;
RA Olsen K.E., Sletten K., Westermarck P.;
RT "Extended analysis of AL-amyloid protein from abdominal wall
RT subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";
RL Biochem. Biophys. Res. Commun. 245:713-716(1998).
CC -!- MISCELLANEOUS: The EU sequence has the INV (3) allotypic marker,
CC 45-Ala and 83-Val. The ROY sequence has the INV (1,2) allotypic
CC marker, 45-Ala and 83-Leu.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; J00241; AAA58989.1; -.
CC EMBL; V00557; CAA23823.1; -.
CC PIR; B90562; K3HU.
CC PDB; 1D5B; 09-FEB-00.
CC PDB; 1D5I; 09-FEB-00.
CC PDB; 1D6V; 04-OCT-00.
CC PDB; 1HEZ; 18-JUL-03.
CC PDB; 1HKL; 12-MAR-97.
CC PDB; 1I7Z; 08-AUG-01.
CC PDB; 1MIM; 15-MAY-97.
CC PDB; 1GNC; 5716; IGKC.
CC MIM; 14720; -.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00047; ig; 1.
CC SMART; SM00407; IGc1; 1.
CC PROSITE; PS50835; IG LIKE; 1.
CC PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT NON_TER 1 102 IG-LIKE.
FT DOMAIN 5 102
FT DISULFID 26 86
FT DISULFID 106 106
FT VARIANT 83 83
FT CONFLICT 14 14
FT CONFLICT 57 57 D -> N (IN REF. 7 AND 8).
FT SEQUENCE 106 AA; 11609 MW; 51984D1FDD372CE8 CRC64; E -> Q (IN REF. 5 AND 6).
Query Match 48.3%; Score 548; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 7.5e-39;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 113 TVAAPSVFIFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDS 172

Db 1 TVAAPSVFIFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDS 60
QY 173 KDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 218
Db 61 KDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 106
RESULT 2
KV1H_HUMAN STANDARD; PRT; 108 AA.
ID KV1H_HUMAN
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT subgroups.";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC PIR; A01868; K1HUHU.
CC HSSP; P80362; 1WTL.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; ig; 1.
CC SMART; SM00406; IGv; 1.
CC PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;
Query Match 41.5%; Score 471; DB 1; Length 108;
Best Local Similarity 82.1%; Pred. No. 1.8e-32;
Matches 92; Conservative 10; Mismatches 6; Indels 4; Gaps 1;
QY 1 DIQLTQSPSSLSASVGRVTITCRASQSDYDGDSDYMNWYQQKPKAPKLLIYAASYLES 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSI-----SSYLSWYQQKPKAPQVLIYAASSLPS 56
QY 61 GVPSRFRSGSGGTDFLTITSLQPEDFATYCCQSHEDPYTFGQGTKVEIKR 112
Db 57 GVPSRFRSGSGGTDFLTITSLQPEDFATYCCQNYITPTSFQGTTRVEIKR 108
RESULT 3
KV3M_MOUSE STANDARD; PRT; 111 AA.
ID KV3M_MOUSE
AC P01665;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7043.

```
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.B.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR; A01937; KVM543.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON TER 111
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 41.1%; Score 467; DB 1; Length 111;
Best Local Similarity 77.5%; Pred. No. 4.1e-32;
Matches 86; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRVTITCRASQSVYDGDSDSYMNWYQQKPGKAPKLLIYAASYLE 60
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSVYDGDSDSYMNWYQQKPGQPPLIYAASNLES 60

QY 61 GVPSPRFGSGSGTDFLTITSSLOPEDFATYYCQSHEDPYTFGQGTKVEIK 111
Db 61 GIPARFSGSGSGTDFLTINHPVEEDAATYYCQSNEDPFTFGSGTKLEIK 111

RESULT 4
KV1E HUMAN
ID KV1E_HUMAN STANDARD; PRT; 108 AA.
AC P01597;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region DEE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72053133; PubMed=5124396;
RA Milstein C.P., Deverson E.V.;
RT "The amino acid sequence of a human kappa light chain.";
RL Biochem. J. 123:945-958(1971).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR PIR; A01865; KIHUDE.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
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FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON TER 108
SQ SEQUENCE 108 AA; 11661 MW; BDD6E350017F1E51 CRC64;

Query Match 40.8%; Score 463; DB 1; Length 108;
Best Local Similarity 79.5%; Pred. No. 8.4e-32;
Matches 89; Conservative 10; Mismatches 9; Indels 4; Gaps 1;

QY 1 DIQLTQSPSSLSASVGDRVTITCRASQSVYDGDSDSYMNWYQQKPGKAPKLLIYAASYLE 60
Db 1 BIZMTQSPSSLSASVGDRVTITCRAGQSV----NKYLNWYQQKPGKAPKVLIFAASSLKS 56

QY 61 GVPSPRFGSGSGTDFLTITSSLOPEDFATYYCQSHEDPYTFGQGTKVEIKR 112
Db 57 GVPSPRFGSGSGTDFLTITISGLLPEDFATYYCQSYTTPYTFGPGTKVENTR 108

RESULT 5
KV3O MOUSE
ID KV3O_MOUSE STANDARD; PRT; 111 AA.
AC P01667;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 6308.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR; C01937; KVM508.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON TER 111
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 40.7%; Score 462; DB 1; Length 111;
Best Local Similarity 76.6%; Pred. No. 1.1e-31;
Matches 85; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRVTITCRASQSVYDGDSDSYMNWYQQKPGKAPKLLIYAASYLE 60
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSVYDGDSDSYMNWYQQKPGQPPLIYTASNLES 60

QY 61 GVPSPRFGSGSGTDFLTITSSLOPEDFATYYCQSHEDPYTFGQGTKVEIK 111
Db 61 GIPARFSGSGSGTDFLTINHPVEEDAATYYCQSNEDPFTFGSGTKLEIK 111
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RESULT 6
KV3N MOUSE
ID_KV3N MOUSE STANDARD; PRT; 111 AA.
AC P01666;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7183.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; B01937; KVM583.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

Query Match 40.5%; Score 460; DB 1; Length 111;
Best Local Similarity 76.6%; Pred. No. 1.5e-31;
Matches 85; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITTCRASQSVYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
DB 1 DIVLTQSPASISVLSGLQRTATISCKASQSVYDGDSDYNNWYQKPGQPPKLLIYAASNLE 60

QY 61 GVPSRFGSGSGTDFTLTISLQPEDFATYCCQSHEDPYTFGQGTKEIK 111
DB 61 GIPARFSGSGSGTDFTLNHPVEEDAATYCCQSNEDPLTFGAGTKLELK 111

RESULT 7
KV1W HUMAN
ID_KV1W HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobeck H.G., Combriato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
KW
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CC -----
CC EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01883; K1HUKW.
DR HSSP; P01607; 1REI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match 40.5%; Score 460; DB 1; Length 129;
Best Local Similarity 82.0%; Pred. No. 1.9e-31;
Matches 91; Conservative 8; Mismatches 8; Indels 4; Gaps 1;

QY 1 DIQLTQSPSSLSASVGDRTVITTCRASQSVYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
DB 23 DIQMTQSPSSLSASVGDRTVITTCRASQSI-----SNYLNWYQKPGKAPKLLIYAASLS 78

QY 61 GVPSRFGSGSGTDFTLTISLQPEDFATYCCQSHEDPYTFGQGTKEIK 111
DB 79 GVTSRFGSGSGTDFTLTISLQPEDSATYCCQSYSTLITFGQGTREIK 129

RESULT 8
KV3Q MOUSE
ID_KV3Q MOUSE STANDARD; PRT; 111 AA.
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7769.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; E01937; KVM569.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
```


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OM protein - protein search, using sw model

Run on: May 13, 2004, 15:36:43 ; Search time 23.392 Seconds
(without alignments)
2940.454 Million cell updates/sec

Title: US-09-925-179-9
Perfect score: 1135
Sequence: 1 DIQLTQSPSSLSASVGRVT.....EVTHQGLSSPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL 25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	988	87.0	234	4 Q7Z473	Q7z473 homo sapien
2	988	87.0	236	4 Q7Z3Y4	Q7z3y4 homo sapien
3	892.5	78.6	239	4 Q8NEK0	Q8nek0 homo sapien
4	891.5	78.5	239	4 Q8TCD0	Q8tcd0 homo sapien
5	738	65.0	234	11 Q8R062	Q8r062 mus musculus
6	738	65.0	236	11 Q7TMK3	Q7tmk3 mus musculus
7	733	64.6	234	11 Q91WF8	Q91wf8 mus musculus
8	732	64.5	233	11 Q91WS9	Q91ws9 mus musculus
9	731	64.4	214	11 Q9R1A5	Q9r1a5 mus musculus
10	730	64.3	234	11 Q8VCP0	Q8vcp0 mus musculus
11	723	63.7	236	11 Q7TS98	Q7ts98 mus musculus
12	703.5	62.0	238	11 Q99M37	Q99m37 mus musculus
13	693.5	61.1	238	11 Q8VCI6	Q8vci6 mus musculus
14	693.5	61.1	239	11 Q8VC55	Q8vc55 mus musculus
15	689.5	60.7	235	11 Q7TMK0	Q7tmk0 mus musculus
16	684.5	60.3	235	11 Q91W12	Q91w12 mus musculus

17	679.5	59.9	239	11 Q8K0F8	Q8k0f8 mus musculu
18	662	58.3	234	11 Q8R028	Q8r028 mus musculu
19	590	52.0	237	13 Q7SZ36	Q7sz36 xenopus lae
20	487	42.9	108	4 Q9UL77	Q9ul77 homo sapien
21	475.5	41.9	107	4 Q96SA9	Q96sa9 homo sapien
22	459	40.4	116	4 Q96PF6	Q96pf6 homo sapien
23	450.5	39.7	107	4 Q9UL81	Q9ul81 homo sapien
24	446	39.3	108	4 Q9UL70	Q9ul70 homo sapien
25	445	39.2	236	4 Q8NEJ1	Q8nej1 homo sapien
26	444	39.1	111	11 Q811U6	Q811u6 mus musculu
27	440.5	38.8	237	4 Q8WUK4	Q8wuk4 homo sapien
28	439.5	38.7	233	4 Q8TBC9	Q8tbc9 homo sapien
29	439.5	38.7	237	4 Q8WTU6	Q8wtu6 homo sapien
30	435	38.3	108	4 Q9UL79	Q9ul79 homo sapien
31	422	37.2	234	4 Q8N355	Q8n355 homo sapien
32	413.5	36.4	233	4 Q8N5F4	Q8n5f4 homo sapien
33	413	36.4	111	11 Q920E9	Q920e9 mus musculu
34	403.5	35.6	236	4 Q96E61	Q96e61 homo sapien
35	399	35.2	234	4 Q7Z2U7	Q7z2u7 homo sapien
36	397.5	35.0	235	11 Q99M11	Q99m11 mus musculu
37	395	34.8	230	4 Q7Z2U3	Q7z2u3 homo sapien
38	395	34.8	240	4 Q8WUK3	Q8wuk3 homo sapien
39	391	34.4	298	11 Q9QYF0	Q9qyf0 mus musculu
40	389.5	34.3	112	11 Q8K1F3	Q8k1f3 mus musculu
41	388.5	34.2	114	11 Q8K1F1	Q8k1f1 mus musculu
42	387.5	34.1	109	4 Q9UL78	Q9ul78 homo sapien
43	380	33.5	109	11 Q920E6	Q920e6 mus musculu
44	379.5	33.4	112	11 Q8K1F2	Q8k1f2 mus musculu
45	376	33.1	108	4 Q9UL83	Q9ul83 homo sapien

ALIGNMENTS

RESULT 1

Q7Z473	ID	Q7Z473	PRELIMINARY;	PRT;	234 AA.
AC	Q7Z473;				
DT	01-OCT-2003 (TRENBLrel. 25, Created)				
DT	01-OCT-2003 (TRENBLrel. 25, Last sequence update)				
DT	01-OCT-2003 (TRENBLrel. 25, Last annotation update)				
DE	Hypothetical protein.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Lung;				
RX	MEDLINE=2238257; PubMed=12477932;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schat N.K.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,				
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,				
RA	Jones S.J., Marra M.A.;				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Lung;				

Query Match 65.0%; Score 738; DB 11; Length 236;
Best Local Similarity 63.8%; Pred. No. 2.3e-59;
Matches 139; Conservative 31; Mismatches 44; Indels 4; Gaps 1;

QY 1 DIQLTQSPSSLSASVGDRTVTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Db 23 DIKMTQSPSSMYASLGERVTITCKASQDI---KSYSWYQKPKWSPKTLIYATSLAD 78

QY 61 GVPFRFSGSGSGTDFTLTISSLPQEDFATYQCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
Db 79 GVPFRFSGSGSGDYSLTISLESDDTATYCLQHGESPYTFGGTKLEIKRADAAPTVS 138

QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
Db 139 IFPPSDEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDYSL 198

QY 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNREGC 218
Db 199 STLTLTDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 236

RESULT 7

QY1WF8 PRELIMINARY; PRT; 234 AA.

AC Q91WF8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015292; AAH15292.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR InterPro; IPR001865; Ribosomal_S2.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0B6EB7812D2 CRC64;

Query Match 64.6%; Score 733; DB 11; Length 234;
Best Local Similarity 63.3%; Pred. No. 6.4e-59;
Matches 138; Conservative 31; Mismatches 45; Indels 4; Gaps 1;

QY 1 DIQLTQSPSSLSASVGDRTVTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Db 21 DIQMTQTSSLSASLGDRVTITCRASQDI---SNYLNWYQKPDGTVKLLIYTSRLYL 76

QY 61 GVPFRFSGSGSGTDFTLTISSLPQEDFATYQCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
Db 77 GVPFRFSGSGSGTDYSLTISNLEQEDATYFCQGNTPPTFGSGTKLEVKRADAAPTVS 136

QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
Db 137 IFPPSDEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDYSL 196

QY 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNREGC 218

Db 197 STLTLTDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234

RESULT 8

QY1WS9 PRELIMINARY; PRT; 233 AA.

AC Q91WS9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013496; AAH13496.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match 64.5%; Score 732; DB 11; Length 233;
Best Local Similarity 64.2%; Pred. No. 7.8e-59;
Matches 140; Conservative 28; Mismatches 46; Indels 4; Gaps 1;

QY 1 DIQLTQSPSSLSASVGDRTVTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Db 20 DIQMTQTSSLSASLGDRVTITSCSGQGI---ANYLNWYQKPDGTVKLLIYTSLSL 75

QY 61 GVPFRFSGSGSGTDFTLTISSLPQEDFATYQCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
Db 76 GVPFRFSGSGSGTDYSLTISNLEPEDIATYQCQYRYPWTFGGTKLEIKRADAAPT 135

QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
Db 136 IFPPSDEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDYSL 195

QY 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNREGC 218
Db 196 STLTLTDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 233

RESULT 9

QY1A5 PRELIMINARY; PRT; 214 AA.

AC Q91A5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Kappa light chain of Mab7 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G.; Yu X.; Ekramoddoullah A.K.M.; Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scFV).";
RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.


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RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021781; AAH21781.1; -.
DR PIR; A33933; A33933.
DR PDB; 1KCS; 24-JUL-02.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF02950; Conotoxin; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26303 MW; C16119CACAA25C337 CRC64;

Query Match 61.1%; Score 693.5; DB 11; Length 239;
Best Local Similarity 58.9%; Pred. No. 2.7e-55;
Matches 129; Conservative 38; Mismatches 51; Indels 1; Gaps 1;

QY 1 DIQLTQSPSSLSASVGDRTVITTCRASQS-VDYDGSYMNWYQKPKAPKLLIYAASYLE 59
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 21 DVVLTQTPLSLPNIGDQASISCKSTKSLNSDFTYLDWYLPKPGQSPQLLIYVSNRF 80
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 60 SGVPSRFSGSGGTDFTLTISSLPEDPATYCYQQSHEDPYTFGGTKVEIKRTVAAPSV 119
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 81 SGVPDRFSGSGGTDFTLKISRVEADLGVYCFQSNHLPYTFGGTKLEIKRADAPT 140

QY 120 FIFPPSDEQLKSGTASVVCVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 179
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 141 SIFPPSSEQLTSGGASVVCFLNLFYPKDINVKWKIDGSRQGVLSWTDQDSKDSYSM 200

QY 180 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 201 SSTLTLTKDEYERHNSYTCEATHKSTSTSPIVKSFNRNEC 239

RESULT 15
Q7TMKO PRELIMINARY; PRT; 235 AA.
AC Q7TMKO;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
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RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055911; AAH55911.1; -.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25861 MW; 3EBA0312A87613F4 CRC64;

Query Match 60.7%; Score 689.5; DB 11; Length 235;
Best Local Similarity 60.9%; Pred. No. 6.1e-55;
Matches 131; Conservative 32; Mismatches 47; Indels 5; Gaps 1;

QY 4 LTQSPSSLSASVGDRTVITTCRASQSVDYDGSYMNWYQKPKAPKLLIYAASYLESGVP 63
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 26 LTQSPAINMSASLGEKVTMSCRASRV-----NYMYWYQQSGASPKLWIYYTSNLAGVP 80

QY 64 SRFSGSGGTDFTLTISSLPEDPATYCYQQSHEDPYTFGGTKVEIKRTVAAPSVFIFP 123
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 81 ARFSGSGGTSTSLTISSEAEADAATYCYQQSLSTSPWTFGGSKLEIKRADAAPTVSIFP 140

QY 124 PSDEQLKSGTASVVCVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 183
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 141 PSSEQLTSGGASVVCFLNLFYPKDINVKWKIDGSRQGVLSWTDQDSKDSYMSSTL 200

QY 184 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
   ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 201 TLTKEYERHNSYTCEATHKSTSTSPIVKSFNRNEC 235
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Search completed: May 13, 2004, 15:47:22
Job time : 24.392 secs